

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 122814

TO: David Lukton

Location: REM-3B75/3C70

Art Unit: 1653

Tuesday, May 25, 2004

Case Serial Number: 09/594978

From: Toby Port

Location: Biotech-Chem Library

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Lukton,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port



Peptide #
Human liv
Human pep
Streptoco
Human imm
Human imm
Human imm
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Human imm

Aam33910 Abg55464 Abg43601 Aaw62760 Aam82654 Human agu Tbp2 anti Human agu H. influe UDP-N-ace

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ABMS0073
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ABM41988
ABP62931
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AAX7953
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Aau25148 Obpicable
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Aav78909 MAGB 310
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ALIGNMENTS

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AAM47151 standard; peptide; 6 AA.
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12-FEB-2002 (first entry)

S chrysomallus actinomycin biosynthase protein acmC fragment #9.

Modular enzyme system; cyclic gene synthesis; repetitive coding sequence; antibiotic; non-ribosomal peptide synthetase; NRPS; PKS; polyketide synthase; actinomycin biosynthase.

Streptomyces chrysomallus

Synthetic

WO200181564-A2.

01-NOV-2001.

25-APR-2001; 2001WO-DE001578

26-APR-2000; 2000DE-01021267

(ACTI-) ACTINODRUG PHARM GMBH

Schauwecker F;

WPI; 2002-049276/06. N-PSDB; ABA03345.

Preparing DNA encoding modular protein for e.g. producing new enzymes for synthesis of polyketide antibiotics, comprises cyclic integration of fragments into a vector.

Example 3; Page 54; 83pp; German.

The present invention relates to the preparation of DNA, in a circular vector, that encodes one or more segments of a modular polypeptide. DNA or DNA libraries produced this way are used to produce modular polypeptides, particularly enzymes, which can be used to act on

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substrates to produce compounds for therapeutic testing. Bnzymes of particular interest are those involved in non-ribosomal peptide synthesis or polyketide synthesis, and compounds for testing are particularly macrolide antibiotics, including penicillins, vancomycins or erythromycins, but may also be modular receptors. The present sequence is a fragment of a protein encoded by a Streptomyces chrysomallus actinomycin biosynthesis gene which was used in a plasmid in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. It ike parthology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
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amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
inhibitor.
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Tung J, Wang S, Mcconlogue L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-secretase, beta-amyloid precursor protein, beta-amyloid peptide, amyloid plaque component, Alzheimer's disease, amyloidogenic disease; inhibitor.
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Wang S, Mcconlogue L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-2000; 2000WO-US003819.
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99US-0139172P
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                              4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tatsuno G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-533011/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease
Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                                                                     1 VAEF 4
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Modified-site
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15-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                    AAB07872;
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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onest or course of VD, especially detecting in a sample of cerebrospinal fluid (CSP) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stege of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
                                                                                                                                                                                                                                                                                                    VD; VD-associated protein isoform; VPI; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                        Vascular dementia-associated protein isoform (VPI) 441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
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                                                                                                                                                                                                                                                                                                                                         diagnosis; prognosis; gene therapy
ABB56241 standard; peptide; 8 AA.
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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                                                                                                                                                                                                                                                                                                Vascular Dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                15-FEB-2002
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The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest peptides of these proteins. Some of the DPIs (AAU28404-AAU28625) described are decreased in the cerebrospinal fluid (CSF) of BAD (Bipolar affective disorder) subjects, whilst other DPIs (AAU28625-AAU28887) are increased in BAD subjects, whilst other DPIs (AAU28625-AAU28887) are identified from DPI-45 and DPI-213 and the nucleic acid sequence they are socioded by. The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, schizoaffective disorders, attention deficit disorders. The present sequence represents one of the DPI tryptic digest peptides of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
                                               Human; depression associated protein isoform; tryptic digest peptide; DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder; neuropsychiatric disorder; bipolar mood disorder; neuroleptic; maniac-depressive illness; schizoaffective disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizophrenia-Associated Protein Isoform (SPI) peptide #343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 37; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                       (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
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                DPI tryptic digest peptide #317
                                                                                                                                                                                                                                                                               24-FEB-2000; 2000GB-0004412.
08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
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Best Local Similarity
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                                                                                                                                       Homo sapiens.
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Tyson KL;

Terrett JA,

Rohlff C,

Gaps ö

Length 8; 0; Indels

100.0%; Score 19; DB 4; I 100.0%; Pred. No. 1.4e+06; Mismatches

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                                                                                                                                                                                                                    New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
                                                                                                                                                                                                                                                                                                        The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SFI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, Bipolar Affective Disorder, BAD; Depression-Associated feature;
DF; Depression-Associated protein isoform; DF; Cerebro-epinal fluid;
CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
attention deficient disorder; schizoaffective disorder;
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                                                                                                                                                           Tyson KL;
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                                                                                                                                                            Terrett JA,
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                                                                                                                                                         Herath HMAC, Parekh RB, Rohlff C,
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                                                                                                                                                                                                                                                                                Disclosure, Page 36, 148pp, English.
                                                                                                                              (OXFO-) OXFORD GLYCOSCIENCES UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rohlff C;
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
                                                                                    24-FEB-2000; 2000GB-00004415.
28-DEC-2000; 2000US-00750395.
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                                                         23-FEB-2001; 2001WO-GB000792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unipolar affective disorder
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                                                                                                                                                                                         WPI; 2001-570624/64
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WO200162785-A2
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08-DEC-2000;
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                            30-AUG-2001
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Matches
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Query Match
Best Local Similarity
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Sequence 8 AA;
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                                                  Matches
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The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH. Associated Protein Isoforms (SPIS) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential therapeutic agents. The method is used for (1) screening or diagnosis of SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH; and (2) monitoring the effect of therapy administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFs, SPIs and related molecules (e.g. secondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment and as targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes neuropsychiatric disorders such as SCH from neurological disorders, where manifestations of anatomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropathies are necessary for improved treatment of section and characterisation of cellular and/or molecular causative defects and neuropathies are necessary for improved treatment of sections of schizophrenia-associated contracts and the processory is the animon of defects and neuropathies are necessary for improved treatment of sections of schizophrenia-associated contracts and the processory is the processor of sequences of schizophrenia-associated contracts and the processor of sequences of schizophrenia-associated contracts and the processor of sequences of schizophrenia-associated contracts and the processor of sequences of schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A compsn. which induces a cytotoxic T lymphocyte (CTL) response to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compsn. inducing cytotoxic T lymphocyte response to pref. viral, bacterial, parasitic or tumour antigens - useful in the treatment prevention of diseases associated with the antigen e.g. hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 19; DB 4; I 100.0%; Pred. No. 1.4e+06; Live 0; Mismatches 0;
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(first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
27-MAR-1996
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                                                                                                                                                                                                                               The invention relates to a preparation comprising an isolated Bipolar Affected Disorder (BAD)-Associated Protein Isoform (DPIS). The DPI's are used to screen, diagnose or prognose of BAD or unipolar depression, identify a cutrant of the stage or severity of BAD or unipolar depression, identify a subject at risk of developing BAD or unipolar depression, or monitor the cffect of therapy in a subject. They are also used to screen for or identify agents that interact with a DPI. These agents, antibodies against the DPIs, and nucleic acids encoding the DPIs are used to treat or prevent BAD or unipolar depression. Diseases that can be treated are attention deficient disorder. As expiracaffective disorder, a bipolar or a unipolar affective disorder. The DPIs are used in proteomics. The BAD or unipolar depression overcomes the problems of using gene expression analysis, such as not being able to obtain central nervous greent compact of a DPI increased in the CSF (cerebro-spinal fluid) of subjects having BAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                         ö
                                                                Preparation for diagnosing or treating bipolar affected disorder (BAD) unipolar depression, or for screening for modulators, comprises a BAD-associated protein isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Peatures and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizophrenia-associated isoform peptide #343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rohlff C;
                                                                                                                                                                                 Claim 8; Page 37; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU15458 standard; peptide; 8 AA.
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28-DEC-2000; 2000US-00750395
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         WPI; 2001-582081/65.
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Grey H;

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Length 8; Indels us-09-594-978a-2.rag

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Gaps

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Length 9; Indels

Score 19; DB 5; L. Pred. No. 1.4e+06; 0; Mismatches 0;

100.0%; ilarity 100.0%; Conservative 0

Query Match Best Local Similarity

6 VAEF

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enzyme; cleavage site; amyloid protein precursor; APP; se; neuroprotective; nootropic; beta-secretase inhibitor;

Beta-secretase related peptide SEQ ID NO:197.

aspartyl protease; r Alzheimer's disease

Homo sapiens

Synthetic.

31-MAY-2002 (first entry)

ABB06593;

ABB06593 standard; peptide; 10 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crystallized complex of beta-site amyloid precursor protein (APP) cleaving enzyme (BACE) and APP inhibitor peptide useful for identifying agents that interact with active site of BACE or active site of APP
human MAGE antigen (Ag) in a mammal comprises, a MAGE CTL Ag response inducing peptide (i.e. AAR78904 to AAR78917) and a lipid conjugated helper T cell inducing peptide. The compsn. is useful in the treatment and prevention of MAGE tumour Ag associated diseases, e.g. melanoma cancers. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                  Beta-amyloid precursor protein, APP, APP inhibitor peptide, BACE, beta site APP cleaving enzyme; protein coordinate data; APP751; Swedish family mutation; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stahl ML
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                                                                                                   100.0%; Score 19; DB 2; Length 9; 100.0%; Pred. No. 1.4e+06; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                          A beta-amyloid precursor protein (APP) inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Svenson K, Annis B, Akopian TN, Bard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                               ABB77871 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding protein or peptide.
                                                                                                                                                                                                                                                                                               27-SEP-2002 (first entry)
                                                                                                                               4; Conservative
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                                                                                                     Query Match
Best Local Similarity
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Misc-difference
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                                                                            Sequence 9 AA;
                                                                                                                                                                                2 VAEF
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Somers WS;
                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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ABB77871
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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 188; 188pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 AA;
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The present sequence represents a beta-amyloid precursor protein (APP) inhibitor peptide. This peptide inhibits binding between APP and BACE lebta site APP cleaving enzyme). The specification describes a crystallized complex of BACE and the present APP inhibitor. Protein coordinate data for BACE is given in the specification. The APP inhibitor peptide is based on the P10 to P4' APP751 Swedish family mutation. The crystallized complex is used for identifying an agent that interacts with an active site of BACE or an active site of an APP binding protein or peptide. The agents are useful in the treatment and/or prevention of

Novel substrates for human aspartyl protease useful for identifying modulators of beta secretase activity of aspartyl protease for treating

Alzheimer's disease.

Bienkowski MJ;

Emmons TL,

Gurney ME,

Tomasselli AG,

Heinrikson RL;

Yan R,

WPI; 2002-216995/27.

(PHAA) PHARMACIA & UPJOHN CO

19-JUL-2001; 2001WO-US023035. 19-JUL-2000; 2000US-0219795P. 12-MAR-2001; 2001US-0275251P.

WO200206306-A2.

24-JAN-2002

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The invention relates to an inhibitor of catalytically active memapsin 2 can aspartic protease which can cleave at beta secretase sites), which binds to the active site of memapsin 2 defined by the presence of two catalytic aspartic residues and substrate binding cleft. Also included is a method of determination of the substrate binding cleft. Also included is nemapsin 2 sub-sites comprising: (a) reacting a maxture of memapsin 2 sub-sites comprising: (a) reacting a maxture of memapsin 2 substrates; or (b) preparing a combinatorial mixture of memapsin 2 substrates; or (c) preparing a combinatorial library of memapsin 2 inhibitors containing a base sequence taken from MM99-2 (du-val-Asn-leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 which binds to several inhibitors to generate secondary antibody. The inhibitors may be used in the manufacture of a medicament for the treatment of Alzheimer's disease since memapsin 2 may be involved in the cleavage of amyloid precursor protein (APP), and for the present sequence represents a substrate purchant perference in memapsin 2 sub-sites. The present sequence represents a substrate perference in memapsin 2 sub-sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
                                                                                 Human; memapsin 2; aspartic protease; beta secretase; degenerative disease; Alzheimer's disease; amyloid precursor protein; APP; neuroprotective; nootropic; inhibitor; substrate side-chain preference.
                                           Memapsin 2 substrate specificity determination peptide #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 determine the substrate specificity of human memapsin 2
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100.0%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ghosh AK;
                                                                                                                                                                                                                                                                                                                                                                28-DEC-2001; 2001WO-US050826.
                                                                                                                                                                                                                                                                                                                                                                                                           28-DEC-2000; 2000US-0258705P
                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-2001; 2001US-0275756P
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang JJN, Koelsch G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-619088/66
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                                                                                                                                                                                                      sapiens
15-NOV-2002
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                                                                                                                                                                                                                                                                                                                    .1-JUL-2002.
                                                                                                                                                                                                                              Synthetic.
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Best Local S
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                                                                                                                                                                                                                                                                Beta-secretage; enzyme; cleavage site; amyloid protein precursor; APP; aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secretase activity. (I) is useful for identifying agents that modulate the activity of human Asp2 aspartyl procease (Hu-Asp2). (I) is useful as a core structure to construct derivatives. ABL49914 to ABL49925 and ABB06409 to ABB06593 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated peptide (I) comprising a sequence of at least four amino acids, where the peptide is a substrate for conducting aspartyl protease assays. (I) has neuroprotective and nootropic activities, and can be used as an inhibitor of beta-secretase activity. A beta-secretase modulator from the present invention can be used for inhibiting beta-secretase activity in vivo, and in the manufacture of a medicament for the treatment of Alzheimer's disease. Pharmaceutical compositions from the present invention can be used for treating a disease or condition characterised by an abnormal beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel substrates for human aspartyl protease useful for identifying modulators of beta secretase activity of aspartyl protease for treating
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                                                                                                                                                                                                                       Beta-secretase related peptide SEQ ID NO:196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 188; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurney ME,
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                                                                                   ABB06592 standard; peptide; 12 AA.
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12-MAR-2001; 2001US-0275251P.
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                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-216995/27.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                sapiens.
                                                                                                                                                                            31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                 ABB06592;
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Gaps

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BG78404

Length 12; 0; Indels Ξ Power

on N, John V, Mcconlogue L,

Frigon N,

Doane MT, Frigo-

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Tung J,

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The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. Is they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                    Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 33; Page 24; 121pp; English.
                                                                                                                                                                        10-FEB-2000; 2000WO-US003819.
                                                                                                                                                                                                               99US-0119571P.
99US-0139172P.
                                                                                                                                                                                                                                                                                 (BLAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                                                                         Anderson JP, Basi G,
Sinha S, Tatsuno G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-533011/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13 AA;
                                                                                    WO200047618-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200170772-A2
                                                                                                                                                                                                               10-FEB-1999;
                                                                                                                                                                                                                                       15-JUN-1999;
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                                                                                                                              17-AUG-2000
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                                            Synthetic
inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM99276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Awrey D, Beattie B;
' K, Necakov S, Nethery K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises a crystallised recombinant protein that is involved in general metabolism, the recombinant protein may be from Staphylococcus aureus, Streptococcus pneumoniae, Helicobacter pylori, Escherichia coli or Pseudomonas aeruginosa. The crystallised recombinant protein of the invention is useful in the prevention (vaccine) or treatment of a disease or disorder caused by S. pneumoniae, H. pylori, E. coli or P. aeruginosa. The present amino acid sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae, Helicobacter pylori or Pseudomonas aeruginosa involved in general metabolism, useful as drug targets for pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                       crystallised recombinant protein; metabolism; Staphylococcus aureus; Streptococcus pneumoniae; Helicobacter pylori; Escherichia coli; Pseudomonas aeruginosa; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 edadi M, Alam MZ, Awrey l
Houston S, Mansoury K, N
k B, Vallee F, Wrezel O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 66; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A beta-secretase inhibitor peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB07889 standard; peptide; 13 AA
Escherichia coli DnaK peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canadien V, Domagala M, Housto
Ng I, Pinder B, Sheldrick B,
                                                                                                                                                                                                                                                                                                    2001US-0332160P.
2001US-0333661P.
2001US-0333665P.
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28-DEC-2001; 2001US-0344252P.
28-DEC-2001; 2001US-0343570P.
28-DEC-2001; 2001US-0343606P.
                                                                                                                                                                                                                                                                                                                                                                   2001US-0341770P.
2001US-0341954P.
2001US-0342003P.
                                                                                                                                                                                                                                                            21-NOV-2002; 2002WO-CA001768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AFFI-) AFFINIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                           Escherichia coli
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                                                                                                                                                                        WO2003044185-A2
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                                                                                                                                                                                                                                                                                                                                                                     18-DEC-2001;
19-DEC-2001;
19-DEC-2001;
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27-NOV-2001;
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NO COCOCOCO COX IN THE LANGE OF THE LANGE OF
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                                                                Gaps
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0
100.0%; Score 19; DB 3; Length 13; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine related MHC ligand peptide SEQ ID NO:379.
                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                             AAM99276 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-2001; 2001WO-FR000872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                 Local Similarity
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WPI; 2001-611470/70
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Best Local Similarity
Klinguer-Hamour C,
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-FEB-2000;
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inhibitor.
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Matches
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neuroprotective, antimicrobial, gene therapy, vaccine, amylase, cancer, amyloid protein, angiopoletin, apoptosis related protein, cadherin, cyclin, polymerase, oncogene, histone, kinase, colony simulating factor, cyclin, polymerase, oncogene, histone, kinase, colony simulating factor, interleukin, G-protein, coupled receptor; kinesin, cytokine, interferon, interleukin, G-protein coupled receptor; thioseterase, inflammation; multifactorial disease, autoimmune disease, infection,
                                                                                                                                                                                                                                         beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid peptide. This components which accumulate in the brains of individuals affiliated with Alzheimer's disease are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. Ilike pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents a peptide derived from beta-amyloid precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer.
                                                                                                                                                                                                                The specification describes a beta-secretase enzyme. The enzyme cleaves
                                                                                                                   Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fmmunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
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                                  Power
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 3; Length 14; 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0; Indels
                              n N, John V,
Mcconlogue L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human peptide #735 encoded by a SNP oligonucleotide.
                                  Frigon N,
                  Doane MT, First-
                                                                                                                                                                                             Disclosure, Page 12, 121pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM97460 standard; peptide; 14 AA.
                                                 Tung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2000; 2000WO-US035498.
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27-DEC-2000; 2000US-00173419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nervous system disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimkets RA, Leach M;
(ELAN-) ELAN PHARM INC
                                Anderson JP, Basi G,
Sinha S, Tatsuno G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
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                                                                                     WPI; 2000-533011/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200147944-A2
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ID AAM9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associated with interactions between MHC and (I), e.g. melanoma and human immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides which can be used in pharmaceutical compounds from the present invention
                                                                                                                                                         Stabilized pharmaceutical containing N-terminal glutamic acid or glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt with strong acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A peptide fragment derived from beta-amyloid precursor protein.
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                                                                                         Goetsch L;
                                                                                         Corvaia N, Beck A,
                                                     (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB07888 standard; peptide; 14 AA.
                                                                                                                                                                                                                                   Claim 9; Page 96; 149pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0119571P.
99US-0139172P.
                  23-MAR-2000; 2000FR-00003711
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Length 15; 0; Indels

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Identifying coding sequence in genomic databases for conducting proteomics business, by using polypeptide sequence information obtained from peptide sequencing projects, especially those using mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for identifying coding sequence in genomic databases, by using polypeptide sequence information obtained from peptide sequencing projects, especially those using mass spectrometers, it is useful for conducting a proteomics business. It is
                   Disclosure; Page 3829; 4143pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana S11 peptide #6
 autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 41; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                AAE32223 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-2001; 2001US-0282551P.
20-APR-2001; 2001US-0285362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MDSP-) MDS PROTEOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-2003 (first entry)
                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
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                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                               Sequence 14 AA;
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also used for establishing a distribution system for distributing the pharmaceutical preparation for sale, and may optionally include establishing a sales group for marketing the pharmaceutical preparation. It is also used for predicting the gene structure, such as intron/exon boundaries, for searching genomic databases for sequences derived from multi-protein complexes e.g. assemblies with a particular function such as splicing, transport or nuclear import or export, for elucidating transient rather than structural complexes (that are involved in sagnalling pathways) and for identifying proteins in cellular organelles. The present sequence is Arabidopsis thaliana peptide used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic peptide; immunogenic epitope; P3A protein; immune response;
                                                                                                                                                                                                                                                                                       Score 19; DB 6; I
Pred. No. 1.9e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic Hepatitis A virus peptide YK-1369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW42944 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                    h 100.0%;
Similarity 100.0%;
4; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-535831/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
Hepatitis A virus.
                                                                                                                                                                                                                                                                                                                                                                                                          VAEF 13
                                                                                                                                                                                                                                                                                                                                                                        1 VAEF 4
                                                                                                                                                                                                                                                  Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody.
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            0000000000000000
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                                                                                   The present invention relates to oligonucleotides (see AAL26793-AAL34659)
encoding polymorphic variants of proteins related to amylases, amyloid
polymorphic serions of proteins, cadherin, cyclin,
polymerase, oncogenes, histones, kinases, colony etimulating factors,
complement related proteins, cytochromes, kinasins, cytokines,
interferons, interleukins, G-protein coupled receptors and thiosesterases.
The present sequence is a peptide encoded by them may be used in the
present sequence is a peptide encoded by them may be used in the
prevention, diagnosis and treatment of diseases associated with
inappropriate expression of the proteins listed above. Disorders that may
be prevented, diagnosed and/or treatment of diseases (e.g. rheumatoid
with a genetic component, such as autoimmune diseases (e.g. rheumatoid
arthitis, multiple sclerosis, diabetes, systemic lupus erythromatosus
and disease), inflammation, cancer (e.g. cancers of the bladder,
brain, breast, colon and kidney, leukaemia), diseases of the nervous
system and an infection of pathogenic organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic database, mass spectrometer; proteomic business; pharmaceutical; nuclear transport; signalling pathway; cellular organelle.
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Peptides AAW42943-46 are immunogenic peptides corresponding to immunogenic epitopes of the Hepatitis A virus (HAV). The peptides are substantially similar to a portion of the amino acid sequence of the P3A protein of HAV corresponding to amino acids 1423-1496. The present peptide is derived from amino acids 1433-1496. The present is 98.5% with acute sera. Compositions containing the peptides can be used to induce an immune response to HAV in a mammal. The peptides can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptides can also be used to make an antibody against HAV by administering the peptide to a mammal
Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                           Claim 33, Page 115; 140pp; English.
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Score 19;

Query Match

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The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antigenic epitopes of the major structural opsid polypeptides or or non-structural polypeptides of HAV with one or more glutamine or non-structural polypeptides of HAV with one or more glutamine correct the presence of antibodies against HAV in mammalian serum, to detect the presence of AHV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting immunolations in mammalian serum and detecting convalescence in a naminolay, to detect or quantify HAV antibodies in mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal Glutamine at the carboxy end of the peptides enhances the IgM antibody reactivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis A virus, HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                                             Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 19; DB 4; Length 21; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                  USSH ) US DEPT HEALTH & HUMAN SERVICES.
                     Synthetic HAV P3A peptide, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Page 108; 130pp; English.
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                                                                                                                                                                                                                                                                                                             99US-0144412P.
                                                                                                                                                                                                                                                                     14-JUL-2000; 2000WO-US019267.
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                              Fields HA, Khudyakov YE;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-112681/12.
                                                                                                                           Hepatitis A virus.
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                                                                                                                                                                                      WO200105824-A2.
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                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides AAW42943-46 are immunogenic peptides corresponding to immunogenic epitops of the Hepatitis A virus (HAN). The peptides are substantially similar to a portion of the amino acid sequence of the P3A protein of HAV corresponding to amino acids 1423-1496. The present peptide is derived from amino acids 1421-1440 and has a reactivity of 63.4% with acute sera. Compositions containing the peptides can be used to induce an immune response to HAV in a mammal. The peptides can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptides can also be used to make an antibody against HAV by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an immune response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal.
                                                                                                                                                                                                                                                                                                                                                                          Immunogenic peptide; immunogenic epitope; P3A protein; immune response;
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                        Gaps
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100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                   Immunogenic Hepatitis A virus peptide YK-1368.
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                                                                                                                                                                                                          AAW42943 standard; peptide; 20 AA.
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                     4; Conservative
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Local Similarity
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                                                             1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                                                  antibody.
                     Matches
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Gaps

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99US-0144412P

Khudyakov YE;

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The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antigenic epitopes of the major structural applypeptides of the major structural applypeptides of molecules at the carboxy end of the peptide. The peptides are used to detect the presence of Antibodies against HAV in mammalian serum, to detect the presence of Antibodies against HAV in mammalian serum, to detect the presence of HAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting in mammal. The peptides are used to detect or quantify HAV antibodies in mammal. The peptides are used to detect or quantify HAV antibodies in samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the IgM antibody reactivity
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                                                                                                                                                                                                                  Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
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                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                      Claim 22; Page 109; 130pp; English.
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                                               14-JUL-2000; 2000WO-US019267
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                               15-JUL-1999;
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                25-JAN-2001.
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                                                                                                                                       The present immunogenic peptide corresponds to an immunogenic epitope of the Hepatitis A virus (HAV). The peptide is substantially similar to a portion of the amino acid sequence of the Pla protein of HAV corresponding to amino acids 1423-1496. Compositions containing the peptide can be used to induce an immune response to HAV in a mammal. The peptide can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptide can also be used to make an also be used to make an antibody against HAV by administering the peptide to a mammal
                                        an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antigenic epitopes of the major structural capsid polypeptides or non-structural polypeptides of HAV with one or more glutamine molecules at the carboxy end of the peptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to the peptide to an antibody, to detect acute phase infection by detecting ISM antibodies in mammalian serum and detecting convalescence in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                  Immunogenic Hepatitis A Virus (HAV) peptide(\theta) - used to induce an :response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal.
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100.0%; Pred. No. 3.3e+02;
ive 0; Mismatches 0;
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                                                                                                              Claim 33; Page 115; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB69465 standard; peptide; 25 AA.
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Gaps

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4; Length 21; 0; Indels

100.0%; Score 19; DB 4; I 100.0%; pred. No. 2.7e+02; ive 0; Mismatches 0;

97WO-US006891 96US-0015644P

Khudyakov YE;

(first entry)

us-09-594-978a-2.rag

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AAM33910 standard; protein; 28 AA.
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Matches 4; Conserv
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                                                                                                                                                                             Homo sapiens.
                                                                        17-OCT-2001
                                                                                                                                                                                                                                      09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 28
AAM33910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide NT71 (AAW17832) was obtd. by trypsin digestion of human liver mevalonate pyrophosphate decarboxylase (MPD) (AAW17831), an enzyme of the cholesterol biosynthetic pathway. The sequence of the peptide was used to design PCTs primers utilised in the amplification of CDMA from a rat liver CDMA library. A rat MPD partial clone was obtd. and used as a probe to screen a human liver CDMA library. A 1800 bp sequence (AAT66464) coding for human MPD was identified
              samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the IgM antibody reactivity
 The peptides are used to detect or quantify HAV antibodies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human mevalonate pyrophosphate decarboxylase coding sequence - used screening for MPD inhibitors, which regulate and control cholesterol
                                                                                                                                                                             Gaps
                                                                                                                                                                             ö
                                                                                                                                            Score 19; DB 4; Length 25; Pred. No. 3.3e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Human mevalonate pyrophosphate decarboxylase peptide NT71
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mevalonate pyrophosphate decarboxylase; MPD; cholesterol
                                                                                                                                                                                                                                                                                                               AAW17832 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 10; 37pp; English
                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0005652P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-EP004394
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huwyler LR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-245104/22.
                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                       3 VAEF 6
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                                                                                                                                                                                                           1 VAEF 4
                                                                                                                   Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toth MJ,
                                                                                                                                                                                                                                                                                                                                               AAW17832;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placente. The probes are useful for antenatal diagnosis of
                                      Peptide #7947 encoded by probe for measuring placental gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, liver, cirrhosis; hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
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                                                                             Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
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100.0%; Pred. No. 3.7e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 34179; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human liver peptide, SEQ ID No 34112.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                   04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
                                                                                                                                                                                                                                                                                                                                                                                     03.AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US000663
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from human placenta. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157273-A2
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Gaps

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Length 28;

100.0%; Score 19; DB 2; Length 28 100.0%; Pred. No. 3.7e+02; tive 0; Mismatches 0; Indels

Conservative

Local Similarity nes 4; Conserv

Best Loc Matches

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Query Match

RESULT 27

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measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe (SENP) (I) for
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 34112; 658pp; English
                                                                                                       26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                   30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                             WPI; 2001-488898/53
                                                                                     04-FEB-2000;
               09-AUG-2001
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Chen W, Rank DR;

Gabe . 0 100.0%; Score 19; DB 4; Length 28; 100.0%; Pred. No. 3.7e+02; Ative 0; Mismatches 0; Indels Sequence 28 AA;

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ABG43601 standard; peptide; 28 AA. RESULT 29 ABG4360

19-AUG-2002 (first entry) ABG43601;

Human peptide encoded by genome-derived single exon probe SEQ ID 33266. Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary hypertension; hyaline membrane disease.

Homo sapiens

WO200186003-A2

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The invention relates to a patially addressable set or shall be computed to the computed of th
                                                                                                                                                                                                                                                                                                                                                                                      Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a spatially-addressable set of single
                                                                                                                                                                                                                                                                                                                                                                                                                   measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID NO 33266; 634pp; English
                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                             2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                               21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                         30-JAN-2001; 2001WO-US000665
                                                                                                                     2000US-0207456P.
                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-114183/15
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                                                                                                                       26-MAY-2000;
                                                                                                                                                           03-AUG-2000;
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Gaps ö Length 28; Indels 100.0%; Score 19; DB 5; 100.0%; Pred. No. 3.7e+02; iive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 4; Conservative

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2000US-018464P-
2000US-018464P-
2000US-018834P-
2000US-0190076P-
2000US-0190076P-
2000US-019133P-
2000US-020515P-
2000US-020515P-
2000US-0214886P-
2000US-0214886P-
2000US-0214886P-
2000US-0214886P-
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                      2001WO-US001354
                                                                                                                   18-APR-2000; 2
19-MAY-2000; 2
07-JUN-2000; 2
28-JUN-2000; 2
30-JUN-2000; 2
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11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
                      17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a Streptococcal polypeptide. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, maningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                 Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO;
Zarfos PN;
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                                                                                                                                  Polypeptide; ORF; open reading frame; infection; bacterial; streptococcal; bacteremia; diagnosis; prophylaxis.
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100.0%; Score 19; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen SEQ ID NO:10247,
                                                                                                           Streptococcus pneumoniae polypeptide.
                                  AAW62760 standard; protein; 30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM82654 standard; protein; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 32; 181pp; English
                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                      96US-0031879P.
                                                                                                                                                                                                                                               97WO-US021976
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                                                                                   (first entry)
                                                                                                                                                                       Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-322654/28
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                                                                                   09-NOV-1998
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Reid RH, 2
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                                                          AAW62760;
           ESULT 30
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2000US-0249218P
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08-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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(HUMA-) HUMAN GENOME SCI INC.

Barash SC, Ruben SM;

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) amino acid sequences given in AAM82170 to AAW91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polymuclectides may be used to produce the secreted (1), by inserting the protein. (1) proteins and polymuclectides may be used to produce the secreted (1), by inserting the protein. (1) proteins and polymuclectides may be used to provent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic artical general provent, and the present human immune/haematopoietic artical general provents.

Concern the present invention. AAK54921 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention ö Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders. Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis. Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation. Gaps ., Claim 20; SEQ ID NO 22916; 1399pp + Sequence Listing; English Claim 11; SEQ ID NO 10247; 3071pp + Sequence Listing; English Query Match 100.0%; Score 19; DB 4; Length 32; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels Human polypeptide SEQ ID NO 22916. AA009024 standard; protein; 33 AA. 28-FEB-2000; 2000US-00515126. 18-MAY-2000; 2000US-00577409. 26-FEB-2001; 2001WO-US004927 Tang YT, Liu C, Drmanac RT 06-NOV-2001 (first entry) WPI; 2001-514838/56. (HYSE-) HYSEQ INC N-PSDB; AAK55435 N-PSDB; AAI88955 13 VAEF 16 1 VAEF 4 Sequence 32 AA; WO200164835-A2. Homo sapiens. 07-SEP-2001 AAC09024; RESULT 32 AAO09024 ID AAO ò g

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The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to yvotokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immnomodulatory activity and activity, tissue growth factor activity, immnomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthits and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR77953 standard; peptide; 35 AA.
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Best Local Similarity luv...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VAEF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33 AA;
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29-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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Gaps ö

Length 33;

100.0%; Score 19; DB 4; Length 33 100.0%; Pred. No. 4.4e+02; Vismatches 0; Indels

AAR77933-969 are predicted antigenic peptides derived from conserved regions of the Tbp2 protein from H. influenzae strains Bagan, MinnA, DL63 and non-typable strain PAK12085. The transferrin receptor (TER) operon consists of two genes (Tpp1 and Tbp2) arranged in tandem and which are transcribed from a single promoter. H. influenzae TfR is iron- and/or haemin-regulated and a putative fur-binding site has been identified upstream of tbp2. Antibodies blocking this binding site may prevent bacterial growth. Fragments of the TfR (or its genes) are useful in advantage to provide protection against, e.g. bacterial maningitis. An advantage of using the TfR is that it shares homology with TfR of other Nucleic acids encoding Haemophilus transferrin receptor - used to develop prods for detection and in diagnosis, prevention and treatment of Haemophilus infection. Gray-Owen S; Tbp1, Tbp2, transferrin receptor operon; vaccine, antigen; non-typable strain, Haemophilus influenzae, meningitis. Chong P, Schryvers A, Example 16; Page 72; 231pp; English. Antigenic Tbp2 peptide TBP2-21 94WO-CA000616 93US-00148968 93US-00175116 Loosmore S, Harkness R, Sc Yang Y, Murdin A, Klein M, (CONN-) CONNAUGHT LAB LTD. (first entry) WPI; 1995-194089/25

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AAW46126-62 are predicted antigenic peptides derived from the Tbp2 protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin receptor, of which Tbp1 is also a subunit. The deduced amino acid sequences of Tbp1 and Tbp2 were compared, and regions of conservation identified. The above peptides are derived from these regions, the present peptide being derived from these regions, the mustrant for the growth of these bacteria, and they can utilise human transferrin receptor to its iron source prevent bacterial growth. The transferrin receptor, or fragments, therefore, are good vaccine candidates. An immunogenic composition comprising (or encoding) the immunogenic truncated analogue can be used to induce protection against a disease caused by a bacterial pathogen that produces the transferrin receptor. The immunogenic truncated analogue is also useful as an antigen in immunoassays for the detection of Haemophilus transferrin receptor antibodies, while the mucleic acid molecule can be used as antigen antibodies, while the mucleic acid molecule can be used as antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sybridisation probe for the detection of other transferrin receptor genes
H. influenzae strains including non-typable strains. According to the specification the present sequence shows residues 449-484 of Tbp2 from the H. influenzae strain Eagan
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferrin receptor, Haemophilus influenzae type b; iron;
human transferrin; iron source; antibody; bacterial growth; vaccine;
immunogenic truncated analogue; antigen; Tbp1; Tbp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus truncated transferrin receptor protein analogue, Tbp2 - to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gray-Owen S;
                                                                                                                                              o,
                                                                                                           100.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 4.7e+02;
                                                                                                                                              Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chong P,
                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schryvers AB,
                                                                                                                                                                                                                                                                                                                                                                                                                     Predicted antigenic Tbp1 peptide TBP2-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 16; Page 70; 228pp; English
                                                                                                                                                                                                                                                                                                             AAW46146 standard; protein; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harkness RE, Sc
n AD, Klein MH;
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96US-00649518.
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.
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Yang Y, Murdin AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-052329/05.
                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                       14 VAEF 17
                                                                                                                                                                                1 VAEF 4
                                                                          Sequence 35 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
17-MAY-1996;
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                                                                                                             Query Match
                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                          RESULT 34
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RESULT 35 AAY51751

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The present sequence represents the NH2-terminal amino acid sequence of aquaporin-1 (AQP-1), isolated from human erythrocytes. AQP-1 is a water channel proteins regulate the passage of water and out of cells, in response to osmotic changes. The DNA encoding AQP-1 is useful if for the recombinant production of AQP-1, found in mammalian erythrocytes, and is useful in the study to identify reagents which enhance or inhibit water channel function. This can lead to therapeutics which enhance secretion e.g. in the case of dryness of eyes which can lead to blindness or to hydrate large respiratory airways, as their dryness can precipitate asthma
                                                                                                                                                                                                                                                                                                                     /label= Unknown
/note= "not specified but is given as Ser in the full
length protein given in AAW55786"
                                                                                                                                                                 Human, aquaporin-1; AQP-1; water channel protein; regulation; osmotic change; erythrocyte; dryness; blindness; hydration; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide(s) encoding water channel protein Aquaporin-1 for recombinant production of protein for activity studies.
                                                                                                                              Human aquaporin-1 NH2-terminal amino acid sequence CHIP28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 35,
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100.0%; Score 19; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAWS4105 standard; peptide; 35 AA
                      AAW55788 standard, peptide, 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Col 20; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tbp2 antigenic peptide TBP2-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-00468763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-00930168.
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                                                                                               14-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-260501/23.
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                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1995;
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-1992;
24-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                     US5741671-A
                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-1998
                                                                                                                                                                                                             secretion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agre PC;
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AC AAW5
XX
DT 20-C
      AAW55788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel isolated and purified nucleic acid (I) encoding an immunogenic, C-terminally truncated analog of one of the transferrin receptor proteins Thei or Thee of Haemophilus influencae which has antibacterial activity. (I) are used for recombinant production of truncated They; as probes and primers for detecting, and diagnosing tinfection by, Haemophilus, also for isolating similar sequences from other bacteria; as immunogens for vaccinating sainst infections caused by bacteria that produce transferrin receptors, e.g. Haemophilus, Neisseria or Branhamella. The truncated proteins are useful as immunogens (as above); for diagnosing infection (as antigens in immunosasays) and for raising antibodies, used for diagnosis of infections or for passive immunization. AAYS1695-YS1767 represent H. influencae transferrin receptor proteins Tbpl and Tbp2 antigenic peptide fragments
                                                                                                                                                                                                                                                                                                                                                                  Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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to induce protection against disease caused by transferrin producing
pathogens, or as antigen to detect Haemophilus TfR antibodies.
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      Length 35;
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                                    0; Indels
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  Score 19; DB 2; L
Pred. No. 4.7e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                              H. influenzae antigenic Tbp2 peptide TBP2-21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harkness R, Schryvers A,
lein M, Chong P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 16; Col 39-40; 281pp; English.
                                                                                                                                                                                                           AAY51751 standard, protein; 35 AA.
                                        ;
    100.0%;
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93US-00175116.
94US-00337483.
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Query Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-052329/05
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                  17
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                                                                             VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 35 AA;
                                                                                                              14 VAEF
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29-DEC-1993;
08-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6015688-A
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                                                                                                                                                                                                                                                                                                                                                                                       diagnosis.
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                                                                             Н
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Gaps

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Indels

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The invention relates to novel antibodies (or monospecific antisera) specific for single transferrin receptor proteins (or immunogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chong P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä
                                                                                                                                                 Example 2; Col 20; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY80448 standard; peptide; 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-00148968.
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                        (UYJO ) UNIV JOHNS HOPKINS
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                                                                                                                                                                                                                                                                                                                                            4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schryvers A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae
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                                                                              WPI; 1999-152100/13
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tracheobronchitis.
                                                                                                                                                                                                                                                           present invention
                                                                                                                                                                                                                                                                                                                                                                                               14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                       1 VAEF 4
                                                                                                                                                                                                                                                                                        Sequence 35 AA;
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Murdin A, S
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                                                   Agre PC;
                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                 Peptides AAW53086-W53100 and peptides AAW54100-W54122 are derived from the Tbp2 protein is one of two proteins with genes found on the transferrin operon. These peptides can be used along with the genes, DNA sequences and recombinant proteins for diagnosis, immunisation and the generation of diagnostic and immunological reagents. They can also be used to protect from bacteria that produce transferrin
                                                                                                                                                                                                                                                                                                               Purification of recombinant Haemophilus transferrin-binding protein - by solubilising inclusion bodies separated from cell lysate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                               <u>ت</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat, aquaporin-5, AQP5, AQP1, transmembrane water channel protein, major intrinsic protein, MIP, CHIP28.
                                                                                                                                                                                                                                               Chong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                               Yang Y,
          tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis; passive immunisation; transferrin receptor operon.
                                                                                                                                                                                                                                               Harkness R, Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human aquaporin-1 (CHIP28) N-terminal peptide
                                                                                                                                                                                                                                                                                                                                                          Example 16/17; Column 37-38; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW94320 standard; peptide; 35 AA
                                                                                                                                                            93US-00148968.
93US-00175116.
94US-00337483.
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                                                                                                                                                                                                                   (CONN-) CONNAUGHT LAB LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                            S, Klein M,
Schryvers A;
                                                 Haemophilus influenzae
                                                                                                                                                                                                                                                                                        WPI; 1998-100410/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35 AA;
                                                                                                                                                                          29-DEC-1993;
08-NOV-1994;
                                                                                                                                 12-MUL-1995;
                                                                                                                                                             08-NOV-1993;
                                                                                                                                                                                                                                             Gray-Owen S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-1995;
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                                                                             US5708149-A
                                                                                                       13-JAN-1998
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5 (AQPS). The polynucleotide encoding AQPS is useful for producing recombinant AQPS, which can be incorporated into proteoliposomes or cell membrane vosicles which are able to be used in screening assays for water channel agoniets or antagoniets. The present sequence represents the N-terminal peptide from AQP1 (also called CHIP28), from an example of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                            The present invention describes a water channel protein called aquaporin
DNA encoding aquaporin-5 water channel protein - useful for producing recombinant protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial, antiinflammatory; auditory; respiratory; antibody; antiserum; transferrin receptor; immunogen; epitope; otitis media.bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 35;
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100.0%; Pred. No. 4.7e+02;
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            corresponds to an epitope from the H. influenzae transferrin receptor protein TDp2. The antibodies may be used for preventing and treating infections and disorders caused by H. influenzae, including bacterial meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis. The antibodies may also be used detect the presence of H. influenzae proteins in samples according to standard methodologies (e.g. enzyme linked immunosorbant assay (ELISA)) and hence diagnose infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
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                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - use isolate antimicrobial compounds, and in vaccines against S. aureus
 This sequence
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Ward JM;
                                                                                                                                                                                       h Similarity 100.0%; Pred. No. 4.7e+02; 4; Conservative 0; Mismatches 0; Indels
 fragment) from strains of Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
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Rosenberg M,
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                                                                                                                                                                                                                                                                                                                                                                                AAW27782 standard; protein; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 272; 989pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM CORP
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Pratt JM, Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              toxic shock syndrome.
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N-PSDB; AAT83751.
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Best Local Similarity
Matches 4; Conserv
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Misc-difference 34
                                                                                                                                                                                                                                                                                           14 VAEF 17
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                                                                                                                                                         Sequence 35 AA;
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produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome
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                                                                                                                 Gaps
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                                                                                       Length 36;
                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                      Human excretory related polypeptide SEQ ID NO 570.
                                                                                     Score 19; DB 2; I
Pred. No. 4.8e+02;
Mismatches 0;
                                                                                                                                                                                                                            AAM99833 standard; protein; 37 AA.
                                                                                     100.0%; Sc
100.0%; Pr
live 0;
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2000US-0214886P.
2000US-0215135P.
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2000US-0184664P.
2000US-0186350P.
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2000US-0205515P.
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2000US-0216880P.
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                                                                                                                 4; Conservative
                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        excretory system.
                                                                                                                                        1 VAEF 4
                                                                                                                                                                3 VAEF 6
                                                              Sequence 36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                       AAM99833;
                                                                                       Query Match
                                                                                                    Best Loc
Matches
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18 - AUG - 2000) 2000US - 02265279P . 22 - AUG - 2000) 2000US - 0226681P . 22 - AUG - 2000) 2000US - 0226681P . 22 - AUG - 2000) 2000US - 0227109P . 30 - AUG - 2000) 2000US - 0227109P . 30 - AUG - 2000) 2000US - 0229341P . 01 - SEP - 2000) 2000US - 0229341P . 01 - SEP - 2000) 2000US - 0229341P . 01 - SEP - 2000) 2000US - 0229341P . 01 - SEP - 2000) 2000US - 0229341P . 01 - SEP - 2000) 2000US - 0229341P . 02 - SEP - 2000) 2000US - 0229341P . 03 - SEP - 2000) 2000US - 0229341P . 03 - SEP - 2000) 2000US - 0229341P . 04 - SEP - 2000) 2000US - 0229341P . 05 - SEP - 2000) 2000US - 0229341P . 05 - SEP - 2000) 2000US - 0229341P . 06 - SEP - 2000) 2000US - 0229341P . 06 - SEP - 2000) 2000US - 0229341P . 06 - SEP - 2000) 2000US - 0231413P . 06 - SEP - 2000) 2000US - 0231413P . 06 - SEP - 2000) 2000US - 0231413P . 06 - SEP - 2000) 2000US - 0231413P . 06 - SEP - 2000) 2000US - 0231413P . 06 - SEP - 2000) 2000US - 0231413P . 06 - SEP - 2000) 2000US - 0231414P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2000 200US - 0231413P . 07 - SEP - 2000) 2000US - 0231413P . 07 - SEP - 2
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The invention relates to novel excretory system related human polynucleotides (AA199567-AA199503) and the encoded proteins (AAM99594-AA199503) and the encoded proteins (AAM99594-AA199503) and the encoded proteins (AAM99594-CO (AAM9913) useful for perventing, treating or ameliorating medical conditions e.g. by protein or gene therapy, especially disorders related to the excretory system. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic caids, proteins, cantibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal creates, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, cheumacoid atthritis and ulcerative colitis; (c) cardiovascular disorders such as wrocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases cut as viral, bacterial, fungal and parasitic infections. Once: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. if thy.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding excretory system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; SEQ ID NO 570; 574pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Barash SC, Ruben SM
08-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920BP.
17-NOV-2000; 2000US-024921DP.
17-NOV-2000; 2000US-024921DP.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024939P.
17-NOV-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
19-DEC-2000; 2000US-025198P.
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N-PSDB; AAI98806.
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Gaps .. Query Match
100.0%; Score 19; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels

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14 VAEF 17

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Abwa2648 standard; protein, 37 AA.

Abwa2648;

Abwa2649;

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PR 06-SEP-2000; 2000US-0231434P.
PR 08-SEP-2000; 2000US-0231444P.
PR 08-SEP-2000; 2000US-0231444P.
PR 08-SEP-2000; 2000US-0231444P.
PR 08-SEP-2000; 2000US-0231414P.
PR 14-SEP-2000; 2000US-0231414P.
PR 14-SEP-2000; 2000US-0231414P.
PR 14-SEP-2000; 2000US-023166BP.
PR 25-SEP-2000; 2000US-023166BP.
PR 25-CCT-2000; 2000US-023163BP.
PR 25-SEP-2000; 2000US-023163BP.
PR 25-CCT-2000; 2000US-0231662BP.
PR 25-CCT-2000;
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Peptide #3978 encoded by probe for measuring cervical gene expression.

Probe; human; microarray; gene expression; cervical epithelial cell;

cervical cancer.

Homo sapiens

WO200157278-A2.

09-AUG-2001.

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The invention relates to novel kidney related polynucleotides (AAM2291-AAM3639) and the encoded polypeptides (AAM2417-AAM4659) collectively known as kidney antigens and the use of such kidney antigens for known as kidney antigens and the use of such kidney antigens for cancer metastases. The polynucleotides and proteins are also useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and carciant the specification. The nucleic acids, proteins, antibodies and carciant, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or uregenital, (b) immune disorders e.g. Addison's disease, lung, or uregenital, (b) immune disorders e.g. Addison's disease, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid archaritis and ulcerative collitis; (c) cardiovascular disorders euch as mycardial ischaemias; (d) wound healing, (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, battent did not form parastic infections. Note: The sequence data for the printed specification, but was obtained in electronic format directly from WIPO at the viral, companied format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders.
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100.0%; Pred. No. 5e+02;
ive 0; Mismatches 0; Indels
17-NOV-2000; 2000US-0249297F.
17-NOV-2000; 2000US-0249299F.
17-NOV-2000; 2000US-0249299P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-025031P.
05-DEC-2000; 2000US-0251391P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025199P.
06-DEC-2000; 2000US-025199P.
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08-DEC-2000; 2000US-0251869P
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488784/53
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.

Rank DR;

Chen W,

Hanzel DK,

Penn SG,

WPI; 2001-488901/53

(MOLE-) MOLECULAR DYNAMICS INC

26-MAY-2000; 2000US-0207456P. 30-UUN-2000; 2000US-0060840B. 03-AUG-2000; 2000US-00532366. 27-SEP-2000; 2000US-023466PP. 27-SEP-2000; 2000US-023458PP. 04-OCT-2000; 2000GB-00024263.

30-JAN-2001; 2001WO-US000670

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The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela calls. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; microarray; single exon probe; gene expression; breast; disease;
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB31362;
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WO200157271-A2

09-AUG-2001.

Homo sapiens.

.D AAM17544 standard; protein; 43 AA.

ESULT 43

14 VAEF 17

1 VAEF 4

(first entry)

12-OCT-2001

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the invention research to a specially database set to include the contacting the from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and them measuring the label bound to each probes with human breast, and them measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for session the toxicity of chemical agents on cells. The microarray of this invention presents af ar greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO can feet privation in the published pot sequences.
                                                                                                                                                                                                                                                                                                              New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein #3903 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID NO 14330; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB21904 standard; protein; 43 AA.
                                                                  26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-0508408.
03-AUG-2000; 2000US-00334687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000US-023639P.
                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                30-JAN-2001; 2001WO-US000662
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                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                              WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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                                                    04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
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                                                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45
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ABB21904
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see Ma211535-18A41505). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in \mbox{human} hearts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; SEQ ID NO 23674; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                    Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human liver peptide, SEQ ID No 30062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG51414 standard; peptide; 43 AA
                                                                              26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023458P.
04-OCT-2000; 2000GB-00024263.
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, 2000US-0207456P.
, 2000US-006032366.
, 2000US-0234687P.
, 2000US-0234687P.
, 2000US-0234687P.
                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
30-JAN-2001; 2001WO-US000666.
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                                                        2000US-0180312P
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                                                                                                                                                                                                                                                                                                                                                    Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488899/53
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43 AA;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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ABG51414
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Chen W, Rank DR

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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis.

C hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences
                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #3896 encoded by probe for measuring breast gene expression.
                                                                                                                                                                       Claim 27; SEQ ID NO.30062; 658pp; English.
                                                                                                                                     gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM05214 standard; protein; 43 AA.
               (MOLE-) MOLECULAR DYNAMICS INC.
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                   WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 VAEF 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43 AA;
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                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESULT 47
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X4XHXXXHHXWXOOOOOOOOOOO
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(first entry)

Chen W, Rank DR;

Hanzel DK,

Penn SG,

WPI; 2001-476286/51

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The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one auch probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosting, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention is concerned with producing vaccines against negative stranded RNA viruses. These viruses include measles, respiratory syncytial virus (RSV) and parainfluenza virus (PIV) in particular. The method of the invention comprises the production of a mutated form of the virus which attenuates the strain and enables it to be used as a vaccine. The present sequence comprises a partial viral protein sequence
Novel single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing attenuated negative stranded RNA virus vaccines from cloned sequences, useful for immunizing against e.g. respiratory syncytial virus, human parainfluenza virus, Sendai virus Newcastle disease virus, mumps virus and measles virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Negative stranded RNA virus; vaccine; attenuated virus; RSV; PIV; measles; respiratory syncytial virus; parainfluenza virus.
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                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSV partial protein sequence SEQ ID NO: 26.
                                                          Claim 27; SEQ ID NO 13954; 322pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB27178 standard; protein; 47 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Respiratory syncytial virus.
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 VAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                Sequence 43 AA;
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                          a human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-APR-1999;
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0; Indels

100.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02;

0; Mismatches

ABB37578 standard; peptide; 48 AA.

ABB37578;

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Gaps

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Length 47; Indels

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The present invention relates to human single exon nucleic acid probes (SENP: see AALIO068-AALIO459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human agene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably carvical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #4975 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; microarray; gene expression; cervical epithelial cell;
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                                                       100.0%; Score 19; DB 3; L. 100.0%; Pred. No. 6.4e+02; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                        AAM18541 standard; protein; 48 AA
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0032366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263;
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                              Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                              34 VAEF 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cervical cancer.
                                                                                                                                                                      1 VAEF 4
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Sequence 47 AA;
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Length 48;
        6.6e+02;
hes 0; Indels
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100.0%; Score 19; DB 4;
100.0%; Pred. No. 6.6e+02.
:ive 0; Mismatches 0
                                                                                                             AAM30996 standard; protein; 48 AA.
                                                                                                                                                      17-OCT-2001 (first entry)
                     4; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                      genetic disorder
                                         1 VAEF 4
                                                            VAEF 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #5033 encoded by probe for measuring placental gene expression.
                                                                                                                      Human; foetal liver; gene expression; single exon nucleic acid probe.
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0
                                                                                       Peptide #5084 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 30213; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                            30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236559P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                    WO200157277-A2.
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                                                                                                                                                       Homo sapiens.
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DR;

Rank

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see BAZ1352-BAZ41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
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100.0%; Score 19; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                Claim 15; SEQ ID NO 24638; 530pp; English.
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                 (MOLE-) MOLECULAR DYNAMICS INC.
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30-JUN-2000; 2000US-00608408.
Q3-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234535P.
04-OCT-2000; 2000GB-00024263.
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                                                         Chen W,
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                                                         Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
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                                                                                                                            04-FBB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-05608408.
03-AUG-2000; 2000US-0563356.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
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26-MAY-2000; 2000US-0201456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000GB-00324283.
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Best Local Similarity
Matches 4; Conserv
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                 WO200157272-A2
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us-09-594-978a-2.rag

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. It may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification
                                                 The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
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                 Example 4; SEQ ID NO 30993; 658pp + Sequence Listing; English.
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Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                             ABG52389 standard; peptide; 48 AA.
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; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
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21-SEP-2000; 2000US-0234687P.
2-SEP-2000; 2000US-0233595.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe, human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma
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but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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2000US-0234687P.
2000US-023459P.
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Similarity 100.0%;
4; Conservative 0;
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Matches 4; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                      1 VAEF
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27-SEP-2000;
04-OCT-2000;
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rang YT, Liu C, Drmanac RT;
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18-MAY-2000; 2000US-00577409.
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N-PSDB; AAI85178.
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AAO05247;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferentiation or which may induce production of other cytokines in other cell inpulations. The polymucleotides and polympetides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, hematopoissis regulating activity, issue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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                                                                                                                   AAO10565 standard; protein; 53 AA.
                                                                                                                                                                                                           Human polypeptide SEQ ID NO 24457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT;
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18-MAY-2000; 2000US-00577409.
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Best Local Similarity luv...
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N-PSDB; AAI90496.
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              VAEF
                                         VAEF
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                                                                                                                                                                             06-NOV-2001
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A005247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human polynucleotides (AAI79941-AA193841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                           Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptiddt therapy, stem cell growth factor, haematopoiesis; tissue growth factor, immunomchilatory; cancer, leukaemia; nervous system disorders; arthritis; inflammation.
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Human polypeptide SEQ ID NO 19139.
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17-JAN-2001; 2001WO-US001354
WO200157182-A2
 09-AUG-2001
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2000US-0235836P 2000US-023636P 2000US-023636P 2000US-023636P 2000US-0237037P 2000US-0237037P 2000US-0237037P 2000US-0237038P 2000US-024178F 2000US-024178P 2000US-024652P 2000US-024652P 2000US-024921P 2000US-024924P 2000US-025921P 2000US-025921P 2000US-02598P 2000US-025186P 2000US-025186P 2000US-025189P 2000US-025189P 2000US-025189P 2000US-025189P 2000US-025189P 29-SBP-2000)
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20-CGT-2000)
20-CG

(HUMA-) HUMAN GENOME SCI INC

us-09-594-978a-2.rag

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AMK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) amino acid sequences given in AAW82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polyuncleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient s genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) to polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to provent, (2) proteins and polynucleotides may be used to provent; (3) diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic contains the present human immune/maematopoietic antigen genomic sequences from the present invention. AAK84922 to AAK845950 and AAM82169 represent any of the exemplification of the present invention
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                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human matrix metalloproteinase 7 cleavage region peptide SEQ ID NO:4.
                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 14983; 3071pp + Sequence Listing; English.
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Ruben SM
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21-DEC-2001; 2001US-00032376.
21-MAY-2002; 2002US-00153185.
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   Barash SC,
                                                         WPI; 2001-483426/52
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Best Local Similarity
Matches 4; Conserv
                                                                                      N-PSDB; AAK60171
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Rosen CA,
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BP97126
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The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) comprises an effective amount of a peptide inhibitor of matrix metalloproteinse (WMP), where the peptide can inhibit the expression of VEGF. (I) has cytostatic, vulnerary, cardiant, cerebroprotective, cardiabelic, ophthamological and dermacological activities. (I) can be used for inhibiting expression of VEGF, and so can be used for inhibiting cyrostatic, non-metastatic, vascularised, non-vascularised, hard or soft. (I) is also useful for treating injuries including wounds, surgical inclaions, chronic wounds, heart diseases and stroke. (I) is also useful for treating injuries including wounds, surgical inclaions, chronic wounds, heart diseases and stroke. (I) is also useful for treating disbetic retinopathy. The present sequence represents a human MMP cleavage require which is used in the exemplification of the present invention
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                           Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.
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                                                                                                           Claim 17; Page 15; 103pp; English
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21-DEC-2001; 2001US-00032376.
21-MAY-2002; 2002US-00153185.
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-289980/28.
WPI; 2003-381408/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 VAEF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003016520-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG76312;
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Gaps

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8.1e+02; nes 0; indels

Pred. No. 8.

100.0%; Fit

4; Conservative

Local Similarity

Best Loc Matches

ઠ 셤 ABP04854 standard; protein; 58 AA

ABP04854 ID ABP

RESULT

ABP04854;

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Gaps

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Length 56;

100.0%; Score 19; DB 6; Length 56 100.0%; Pred. No. 7.8e+02; iive 0; Mismatches 0; Indels

Conservative

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The present sequence represents rat PC12 which is used in an example of the present invention which describes protein components of telomerase. The DNA or RNA encoding the telomerase protein component or its fragments can be used as a nucleotide probe for the detection of cancer cells and for diagnosis of cancer. Potential telomerase inhibitors can be screened by measuring their effect on the assay of the active form in cells or tissues. The polypeptide and DNA coding for it can be used in the elucidation of biological control mechanisms of, e.g. cell growth or ageing and of the mechanisms of cancer development
                The present invention relates to peptide inhibitors of metalloproteinases (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have peptide sequences related to the cleavage regions of the proenzyme forms of the MMPS. The peptide inhibitors are useful for stimulating cellular proliferation of fibroblasts or keratinocytes, promoting healthy skin development, treating wounds, preventing scarring, improving skin tone, reducing wrinkling and for simulating the development of smooth, healthy skin. The peptide inhibitors are useful as anti-aging and wound healing compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Telomerase protein of higher animals and humans and gene encoding it for use in diagnosis of cancer, screening of telomerase inhibitors and elucidation of biological control mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; telomerase; human; cancer; screening; inhibitor; elucidation; detection; probe; diagnosis; cell growth; ageing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ishikawa F, Nakamura H, Takahashi K, Fujino Y, Harada N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 69-70; 106pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW55888 standard; protein; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MITU ) MITSUBISHI CHEM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-169149/15.
N-PSDB; AAV25990.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                31 VAEF 34
                                                                                                                                                                                                                                                                                                                          1 VAEF 4
                                                                                                                                                                                                            Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW55888;
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X8888888888888
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(first entry)

96JP-00219761. 97JP-00018878.

97JP-00031807

97WO-JP002904

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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes substantially purified human proteins
                                                                                                                                                                                                                                                                                                                                                                                                               Novel human polypeptides and polymucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autolmmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 9690; 1037pp; English.
                                                        Human ORFX protein sequence SEQ ID NO:9690
                                                                                                                                                                                                                                                                   29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                     29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                           10-MAY-2000; 2000US-0206132P
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                      Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-106308/14.
                                                                                                                                                                     myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABN20606
                                                                                                                                                                                                                     WO200192523-A2
                                                                                                                                                                                               Homo sapiens.
                                  24-JUN-2002
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into present inventions describes subscintary publication invention describes subscintarially publication invention describes subscintarially publication in the specification). ABN15762 to ABN2752 encode the human ORFX in the specification). ABN15762 to ABN2752 encode the human ORFX encodered for proteins given in ABN15762 to ABN2752 encode the human ORFX ensociated disorder in humans, and in the manufacture of a medicament for treating a syderic and are with ORFX associated disorder. ORFX polymuclectide syndrome associated with ORFX ensociated disorder. ORFX polymuclectide squares can be used in the treating of syderic cancer, hyperproliferative disorders, cirrhosis of liver, psorialish, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic ransplantation, cardiovascular diseases, diabetes mellitus, systemic storage disease, various immune disorders and disorders, infectious diseases, autoimmune thypoiditis, myasthenia gravis, graft-versus-host arthritis, autoimmune inflammatory eve disease. And for gut of seases and autoimmune inflammatory evel disease. And for gut of section or regeneration and treatment of lung or liver fibbrosis, repertusion injury in various these and conditions resulting from respection or injury in various these and conditions resulting from systemic cytckine damage. N.B. The sequence date for this patent did not

DB 2;

Score 19;

100.0%;

Query Match

58 AA;

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9908-0137724P

9908-0138094P

9908-0138034P

9908-0139432P

9908-0139453P

9908-014085P

9908-014085P

9908-014085P

9908-0144333P

9908-014598P

9908-014508P

9908-014508P
                                                                                                                                                                                                                                                                                                                           08-JUL-1999;
09-JUL-1999;
12-JUL-1999;
13-JUL-1999;
14-JUL-1999;
15-JUL-1999;
16-JUL-1999;
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22-JUL-1999;
22-JUL-1999;
22-JUL-1999;
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23-JUL-1999;
23-JUL-1999;
23-JUL-1999;
26-JUL-1999;
27-JUL-1999;
                           10 - 70N - 1999)

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19-JUL-1999;
19-JUL-1999;
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20-JUL-1999;
20-JUL-1999;
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27-JUL-1999;
28-JUL-1999;
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                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
 form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                    Gaps
                                                                    .
0
                                               Query Match 100.0%; Score 19; DB 5; Length 58; Best Local Similarity 100.0%; Pred. No. 8.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 77787.
                                                                                                                                                            AAG60085 standard; protein; 59 AA.
                                                                                                                                                                                                                                                                                                                                                           99US-0121825P.
99US-0123180P.
99US-0125788P.
99US-0126788P.
99US-0126788P.
99US-0126788P.
99US-012678P.
99US-012874P.
99US-013081P.
99US-013081P.
99US-013081P.
99US-0131449P.
99US-0131449P.
99US-0132484P.
99US-0134219P.
99US-0134219P.
99US-0134219P.
99US-0134219P.
99US-0134219P.
99US-0134219P.
99US-0134219P.
99US-0134219P.
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                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                         30 VAEF 33
                                                                                       1 VAEF 4
                             Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                            25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
26-MAR-1999;
26-APR-1999;
06-APR-1999;
16-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
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11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
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06-MAY-1999;
06-MAY-1999;
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                                                                                                                                                                                                    18-OCT-2000
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                                                                                                                                                                               AAG60085;
                                                                                                                                        ESULT 63
AG60085
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Gaps ö

Indels

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Score 19; DB 3; Length 59; Pred. No. 8.2e+02;
9904S-0147303P

9904S-0147416P

9904S-0147413P

9904S-0148131P

9904S-0148131P

9904S-0148131P

9904S-0148131P

9904S-0148131P

9904S-0148131P

9904S-0149368P

9904S-0149303P

9904S-0149303P

9904S-0149303P

9904S-0149303P

9904S-0151030P

9904S-01590330P

9904S-01590330P

9904S-01590330P

9904S-01590330P

9904S-01590330P

9904S-01690330P

9904S-0169081P

9904S-0160081P

9904S-0160081P

9904S-0160081P

9904S-0160081P

9904S-0160081P

9904S-016130P

9904S-016130P

9904S-016130P
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99US-0161993P.
99US-0162142P.
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Best Local Similarity
 06-AUG-1999

06-AUG-1999

09-AUG-1999

11-AUG-1999

11-AU
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14-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

21-OCT-1999

21-OCT-1999

21-OCT-1999

22-OCT-1999

22-OCT-1999

22-OCT-1999

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23-OCT-1999

25-OCT-1999

25-OCT-1999

26-OCT-1999

26-OCT-1999
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28-OCT-1999;
29-OCT-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 78631.
Mismatches
                                                                      AAG60683 standard; protein; 59 AA.
ö
                                                                                                                                                                                                                                 9908-0121180P
9908-0123180P
9908-0125788P
9908-0125788P
9908-0125784P
9908-01257452P
9908-0128714P
9908-0128714P
9908-0130891P
9908-0132449P
9908-0132449P
9908-0132489P
9908-0132489P
9908-0132489P
9908-0132489P
9908-0132489P
9908-0134219P
9908-013429P
9908-0135629P
9908-0135629P
9908-0136782P
9908-0136782P
9908-0136782P
9908-0136782P
9908-0136782P
9908-0136782P
9908-0136782P
                                                                                                                                                                                                                   2000EP-00301439
                                                                                                      18-OCT-2000 (first entry)
4; Conservative
                                                                                                                                                                    Arabidopsis thaliana
                              45 VAEF 48
               1 VAEF 4
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08-JUN-1999;
10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
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25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
116-APR-1999;
119-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                                                                                    EP1033405-A2
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06-MAY-1999;
06-MAY-1999;
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                                                                                      AAG60683;
                                                      Matches
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R 16-UW-1999; 99US-019453P.
R 18-UW-1999; 99US-0199453P.
R 23-UW-1999; 99US-014032P.
R 23-UW-1999; 99US-014032P.
R 23-UW-1999; 99US-014032P.
R 23-UW-1999; 99US-014332P.
R 23-UW-1999; 99US-0144332P.
R 23-UW-1999; 99US-0144334P.
R 23-UW-1999; 99US-0144334P.
R 23-UW-1999; 99US-0144334P.
R 23-UW-1999; 99US-0144334P.
R 2
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PR 13-AUC-1999; 9918-01495684P.
PR 17-AUC-1999; 9918-0149368P.
PR 17-AUC-1999; 9918-0149372EP.
PR 20-AUC-1999; 9918-0149372EP.
PR 20-AUC-1999; 9918-0149372EP.
PR 20-AUC-1999; 9918-014932EP.
PR 21-AUC-1999; 9918-015130EP.
PR 21-AUC-1999; 9918-015543EP.
PR 21-AUC-1999; 9918-015593EP.
PR 21-AUC-1999; 9918-015643EP.
PR 21-AUC-1999; 9918-015644EP.
PR 21-AUC-1999; 9918-015644

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Gaps

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1 VAEF

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WO200157272-A2
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                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                          genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #9883 encoded by probe for measuring placental gene expression.
                                                                                             foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                           Peptide #9550 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 34679; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe, microarray, human; placenta, antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 19; DB 4; 100.0%; Pred. No. 8.4e+02;
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                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                      gene expression in human fetal liver.
RESULT 65
ABB42044
ID ABB42044 standard; peptide; 60 AA.
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                                                                                                                                                                                                   26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0033468P.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023458PP.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                       30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                          2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2001 (first entry)
                                                          (first entry)
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Best Local Similarity luv.
                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                        WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 60 AA;
                                                                                                                                   WO200157277-A2
                                                         04-FEB-2002
                                                                                                                 Homo sapiens
                                                                                                                                                                                           04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                        ABB42044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 66
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Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed probe encoded protein SEQ ID NO: 36043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 19; DB 4; Lv 100.0%; Pred. No. 8.4e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 36115; 654pp; English.
                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                           gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM75737 standard; protein; 60 AA.
                                                                          , 2000US-0180312P.
2000US-0207456P.
2000US-00603468.
2000US-00632366.
2000US-0234687P.
2000US-0234687P.
                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
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2000US-00632366.
2000US-0234687P.
2000US-0234687P.
2000US-0234587P.
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                                       30-JAN-2001; 2001WO-US000663
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Best Local Similarity 100...
                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                              WPI; 2001-488897/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 60 AA;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                             21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                04-FEB-2000;
                                                                                                  26-MAY-2000;
                                                                                                                                           03-AUG-2000;
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09-AUG-2001
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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridiese at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease, ABG793910 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent doses not appear in the printed specification but was obtained in electronic format directly from WIPO at
diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, liver, cirrhosis; hyperlipoproteinaemia, hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                    100.0%; Score 19; DB 4; Length 60; 100.0%; Pred. No. 8.4e+02; ive 0; Mismatches 0; Indels
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2000US-00608408.
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21-SEP-2000; 2000US-0234687P
27-SEP-2000; 2000US-0236359P
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                                                                                                                                                                                 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488898/53.
                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                             1 VAEF 4
                                                                                            Sequence 60 AA;
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                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, brain expressed exon, gene expression analysis, probe, microarray, Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy, cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human brain expressed single exon probe encoded protein SEQ ID NO: 35030.
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                                                                                                                                                                                                           Example 4; SEQ ID NO 36043; 658pp + Sequence Listing; English.
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                                                   Rank DR
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       (MOLE-) MOLECULAR DYNAMICS INC
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                                                 Chen W,
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21-SBP-2000; 2000US-0234687P.
27-SBP-2000; 2000US-0235959.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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                                                 Penn SG, Hanzel DK,
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                                                                                            WPI; 2001-488900/53
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 60 AA;
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05-NOV-2001

AAM62925;

SULT 68 M62925

Best Loc Matches

09-AUG-2001

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WO200157182-A2.
                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a human ORF polypeptide, a substrate for extracellular signal-regulated Kinase, ERK-6. Substances that modulate the activity of the ORF polypeptide can be used to treat diseases selected from dermatomyositis, polymyositis, inclusion body myositis, ascoold myopathy, AZT myopathy, myocardial infarction, and ischaemia/reperfusion. The probes and antibodies can be used to detect the presence of ORF in a sample
                                                                                                                                                                                                                                                            ORF polypeptide; dermatomyositis; polymyositis; inclusion body myositis; sarcoid myopathy; AZT myopathy; myocardial infarction; ischaemia; ERK-6; extracellular signal-regulated kinase; reperfusion.
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                         Indels
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100.0%; Pred. No. 8.7e+02;
cive 0; Mismatches 0;
          Pred. No. 8.4e+02;
; Mismatches 0;
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                                                                                                                                                 AAY17262 standard; peptide; 62 AA.
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100.08; Pre
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Best Local Similarity 100.
A; Conservative
                          4; Conservative
                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
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        Best Local Similarity
Matches 4; Conserv
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                                                                             VAEF 11
                                                    1 VAEF 4
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                                                                                                                      RESULT 70
AAY17262
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2000US-0230437P.
2000US-0230438P.
2000US-0231242P.
2000US-0231244P.
2000US-0231244P.
2000US-0231414P.
2000US-0231414P.
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2000US-0218290P.
2000US-0220963P.
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2000US-0227182P.
2000US-0227009P.
2000US-0228924P.
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2000US-0229343P.
2000US-0229344P.
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17-JAN-2001; 2001WO-US001354
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R 25-SEP-2000; 2000US-0225834P.
R 29-SEP-2000; 2000US-0225834P.
R 29-SEP-2000; 2000US-0225834P.
R 29-SEP-2000; 2000US-0225836P.
R 29-SEP-2000; 2000US-022536P.
R 29-SEP-2000; 2000US-022536P.
R 29-SEP-2000; 2000US-022536P.
R 29-SEP-2000; 2000US-022536P.
R 29-SEP-2000; 2000US-022636P.
R 29-SEP-2000; 2000US-022637P.
R 29-CCT-2000; 2000US-022637P.
R 20-CCT-2000; 2000US-022437P.
R 20-CCT-2000; 2000US-0241787P.
R 20-CCT-2000; 2000US-0246474P.
R 20-CCT-2000; 2000US-0246474P.
R 20-CCT-2000; 2000US-0246474P.
R 20-CCT-2000; 2000US-0246478P.
R 20-CCT-2000; 2000US-0246478P.
R 20-CCT-2000; 2000US-0246611P.
R 20-CCT-2000; 2000US-0246622P.
R 20-CCT-2000; 2000US-024662P.
R 20-CCT-2000; 2000US-024926P.
R 20-CCT-2000; 2000US-024929P.
R 20-CCT-2000; 2000US-024929P.
R 20-CCT-2000; 2000US-024929P.
R 20-CCT-2000; 2000
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ANK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) and acid sequences given in AAM92170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) to polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to provent, character immune/haematopoietic-related diseases, sepecially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers and cancer human immune/haematopoietic-derived genomic sequences from the present invention. AAK64942 to AAK54950 and AAM92169 represent sequences used in the exemplification of the present invention
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                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine; immunogenic.
                                                                                                                                                                            Claim 11; SEQ ID NO 18840; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 19; DB 4; Length 62; 100.0%; Pred. No. 8.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic polypeptide #30343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitcham JL, Skeiky YAW, Persing DH, Bhatia A,
Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABM65667 standard; protein; 62 AA.
                                  Ruben SM;
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(HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 100.
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                                  Barash SC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-381789/36.
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                                                                                       N-PSDB; AAK64028
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                                  Rosen CA,
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28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                  06-NOV-2001 (first entry)
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                     07-SEP-2001.
                                                                                                                                                                                          AA009517;
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Specht T, Hinzmann B, WPI; 1999-519629/44. WPI; 2001-514838/56. N-PSDB; AAI89448. 54 VAEF 57 N-PSDB; AAZ33499 1 VAEF 4 Sequence 64 AA; DE19811194-A1 10-MAR-1998; 10-MAR-1998; Homo sapiens 08-DEC-1999 Query Match Best Loci Matches RESULT 74 ઠે The invention relates to an isolated polynucleotide (ACF64415-ACF64731)

encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynuclectides (ARM35624-ARM65365) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polypeptide of the invention; and proteins comprising a polypeptide of the invention; a national proteins comprising a polypeptide of the invention; a national proteins comprising a polypeptide of the invention; a national and an isolated T cell population comprising P. acnes polypeptides, via this method; a vaccine composition (comprising P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in proteins. T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne protein. The polyuncleotides an immune response specific for a P. acnes protein. The polyuncleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the sequence represents a specifically claimed P. acnes polypeptide which is the useful form part of the printed specification, but was obtained in electronic format directly from WIPO at ö polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor; immunomodulatory, cancer; leukaemia, nervous system disorders; arthritis; inflammation. Gaps ö 100.0%; Score 19; DB 6; Length 62; 100.0%; Pred. No. 8.7e+02; ive 0; Mismatches 0; Indels Claim 7; SEQ ID NO 30343; 1481pp; English Human polypeptide SEQ ID NO 23409. AA009517 standard; protein; 64 AA. 4; Conservative

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                                                                                                                                                                                                                         The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynpeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity issue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                            Claim 20; SEQ ID NO 23409; 1399pp + Sequence Listing; English.
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IID AAY4

AAAC AAY4

XXX AAY4

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XXX CADD Homo

XXX CADD

XXX CA
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prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of [I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTS (expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTS. ANY88304-Y48456 represent peptides encoded by the expressed sequence tags described in the method of the invention

Sequence 67 AA;

Gaps ô Length 67; 0; Indels 100.0%; Score 19; DB 2; L 100.0%; Pred. No. 9.4e+02; ive 0; Mismatches 0; Local Similarity 100. Query Match Best Loc Matches

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ESULT 75

ABP31047 standard; protein; 68 AA. BP31047

ABP31047;

(first entry) 08-JUL-2002 Human ORF20 protein, SEQ ID NO:40.

Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; anglogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytuc; tumour inhibition; bodily characteristato; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; noctropic; antipsoriatic; antidiabetic; cytostatic; noctropic; cardiant; hypotensive; antichyoid; antionalmatic; antidiabetic; cytostatic; incorropic; cardiant; hypotensive; antichyoid; antionalmatic; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.

Homo sapiens.

WO200190366-A2.

29-NOV-2001

24-MAY-2001; 2001WO-US017076.

24-MAY-2000; 2000US-0206690P.

(CURA-) CURAGEN CORP.

Leach MD, Shimkets RA;

WPI; 2002-106200/14. N-PSDB; ABN75073. Novel human polypeptides and polymucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation

Claim 10; Page 280; 2508pp; English.

Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses

polypeptides at least 80% identical to the CRFI-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the CRFX motolides at least 85% identical to the CRFX motolides and sequences, vectors and host cells comprising CRFX polynucleotides, the recombinant production of CRFX proteins, antibodies and polynucleotides, the recombinant production of CRFX polynucleotides and cativity, and methods of screening for modulators of ORFX expression or calivity, and methods of screening for modulators of ORFX expression or call differentiation, immune modulation, because of the invention have a wide common that an expectation, and activity, and menocatic activity, heamostatic activity, thrombolytic activity, creeptor/ligand, antiinflammatory activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, thrombolytic activity, creeptor/ligand, antiinflammatory activity, thrombolytic activity, and may also be involved in the determination of bodily characterietics, fertility and behaviour. ORRY proteins, of bodily characterietics, fertility and behaviour. ORRY proteins, of bodily characterietics, fertility and behaviour. ORRY proteins, corber proliferative disorders such as psortiasis and benign tumours, corper proliferative disorders such as psortiasis and benign tumours, neurological disorders uch as epilepsy and Alzheimer's disease.

CC cream ransplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and coholesterol ester fungal and other pathogens. ORRY nuclei acids may also be used as a source of primers and probes, in the decection of ORRY genomic sequences; in genetic diagnosis, and in drug screening. The ORRY proteins may also be useful for studying the function and/or activity of DRFX protein, and in drug screening. The ORRY proteins may also be useful for studying the function activity and useful for studying the function activity and in drug sc

Sequence 68 AA;

. 100.0%; Score 19; DB 5; Length 68; 100.0%; Pred. No. 9.6e+02; 0; Indels 0; Mismatches Ouery Match
Best Local Similarity 100.
Matches 4; Conservative

1 VAEF 4 3 VAEF 6 à d Search completed: May 24, 2004, 17:38:06 Job time : 42.4286 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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May 24, 2004, 17:32:13 ; Search time 10 Seconds (without alignments) 38.477 Million cell updates/sec

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3: pir3:* atabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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peroxisomal target	hypothetical prote	beta-fructofuranos	3-isopropylmalate	dnak-type molecula	hypothetical prote	hypothetical prote	probable thiamin p	drebrin E (clone g	hypothetical prote hera-franctofurance	dnaK-type molecula	hypothetical prote	parasporal crystal	rambrerim-bindin peptidase [importe	hypothetical prote	transferrin-bindin	ATP-dependent bnA hvmothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	propagie chemocasa bacterio-obsin act	hypothetical prote	NADPH-ferrihemopro	growth arrest-spec nentidyl-dinentida	dipeptidyl carboxy	hypothetical prote	hypothetical prote	hypothetical prote	methyl-accepting c	transferrin - Atla	nypornerical ploce conserved hypothet	hypothetical 81.9K	transferrin precur	hypothetical prote	hypothetical prote	asmA protein VC103	carbonic anhydrase	phenylalanine ammo	transferrin precur	phenylalanine ammo	grebiim A - iac large T antigen -	phenylalanine ammo	phenylalanine ammo	phenylalanine ammo	ATP-dependent DNA	phenylalanine ammo	hemolysin secretio	hypothetical prote	fatty-acid oxidati	transforming prote	glycyl-tRNA syntne conserved hypothet	hypothetical prote	probable glgX prot	***************************************
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Ritches, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

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A; Reference number: A64520; MUD:97394467; PMID:9252185

A; Accession: E64618

A; Astatus: preliminary; nucleic acid sequence not shown; translation not shown

A; Residues: 1-48 cTOM>
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: B85745
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE000591; GB:AE000511; NID:g2313918; PIDN:AAD07847.1; PID:g23139;
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C;Accession: A11-1992 #sequence_revision 10-Jul-1992 #text_change 15-Oct-1999
C;Accession: A2375; 139873
B;Ito, K.; Udaka, S.; Yamagata, H.
J. Bacteriol. 174, 2281-2287, 1992
J. Bacteriol. 174, 2281-2287, 1992
A;Ttle: Cloning, characterization, and inactivation of the Bacillus brevis lon gene.
A;Reference number: A42375; MUID:92202157; PMID:1551846
                                                                                                                                                                                                                                                                                                                                         C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: E64618
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                                                                                                                                                                                                                                                                                                    lypothetical protein HP0789 - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 19; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
       Indels
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Best Local Similarity 100.
Matches 4; Conservative
   4; Conservative
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A;Molecule type: DNA
A;Residues: 1-52 <ITO>
                                                                                                                                  15 VAEF 18
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jépecies: Jépecies: Helicobacter jépecies: Helicobacter pylori

jépecies: Helicobacter genome sequence of the gastric pathogen Helicobacter pylori.

jépecies: Jépecies: Jépecies: Helicobacter pylori.

jépecies: Jépecies: Jépecies: Helicobacter pylori.

jépecies: J
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: 839049
R;Lutz, F.; Mohr, M.; Grimmig, M.; Leidolf, R.; Linder, D.
Eur. J. Biochem. 217, 1123-1128, 1993
A;Title: Pseudomonas aeruginosa cytotoxin-binding protein in rabbit erythrocyte membrane
A;Reference number: 839049; MUID:94039134; PMID:7693466
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transforming prote
polysulfide reduct
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DNA polymerase B1
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   probable calcium
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S52990
G84787
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S31816
G96498
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TVHUMB
S23457
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G71308
A69312
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A91038
AF0808
A87516
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4, Molecule type: protein
4, Residues: 1-20 < LUT>
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Best Local Similarity
Matches 4; Conserv
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A,Status: preliminary

4,Cross-references: GB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD07920.1; PID:g23140d

DB 2; Length 33; 88;

Score 19; Pred. No.

100.0%;

Query Match Best Local Similarity

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Gene: Z2382

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R.Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Artile; Wiole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Accession: G64007
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C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 151350
R;Kvingedal, A.M.
Gene 150, 335-339, 1994
A;Title: Characterization of the 5' region of the Atlantic salmon (Salmo salar) transfer: A;Accession: 151350; WUID: 95121925; PMID: 7821802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U32728; GB:L42023; NID:g1573425; PIDN:AAC22109.1; PID:g1573437; T]
                                                                                                                                                                                                                                                                                                        RiArisawa, A.; Tsunekawa, H.; Okamura, K.; Okamoto, R.
Biosci. Biotechnol. Biochem. 59, 582-588, 1995
A;Title: Nucleotide sequence analysis of the carbomycin biosynthetic genes including the
A;Reference number: JC4001; MUID:95290751; PMID:7772821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cassette homology
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A;Rosidues: 1-63 ABN-
A;Cross-references: DDBJ:D30759; NID:g551628; PIDN:BAA06419.1; PID:d1006989;
A;Note: the source was designated as Streptomyces thermotolerans
                                                                                                                                                                                                                 C;Species: Streptomyces sp.
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1999
C;Accession: JC4002
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C.Species: Haemophilus influenzae
C.Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C.Accession: 664007
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                                                                                                                                                                       carbomycin resistance protein carA - Streptomyces sp. (fragment)
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Similarity 100.0%; Score 19; DB 2; Length 63;
8;milarity 100.0%; Pred. No. 1.7e+02;
4; Conservative 0; Mismatches 0; Indels
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Matches 4; Conserv
12 VAEF 15
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Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

Box of the state of the sequence revision 24-Jul-1998 #text_change 05-Nov-1999

Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

Son, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc

180, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Title. Complete genome sequence of Treponema pallidum, the syphilis spirochete.

Reference number: A71250; MuID:98332770; PMID:9655876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klenk, H.P.; Claycon, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. 3lode, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Attre 390, 364-370, 1997.

Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Atth, H.O.; Woese, C.R.; Venter, J.C.

Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec Reference number: A69250; MUID:98049343; PMID:9389475
                                                                Cross-references: GB:AE005174; NID:g12515374; PIDN:AAG56425.1; GSPDB:GN00145; UMGP:Z23; Experimental source: strain 0157:H7, substrain BDL933; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: GB:AE001028; GB:AE000782; NID:g2689351; PIDN:AAB90157.1; PID:g26495d
Superfamily: Methanococcus jannaschii hypothetical protein MJ0975
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Experimental source: strain Nichols
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Species: Archaeoglobus fulgidus
Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jan-2000
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                                                                                                                                                                                                                                               100.0%; Score 19; DB 2; Length 54; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
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100.0%; Score 19; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 4; Conservative
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Residues: 1-59 <KLE>
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Residues: 1-59 < CO
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Genetics: Gene: TP0235

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Cjaccession: F83922 T. Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Mulelic Adids Res. 28, 4317-431, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
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                                                                                                                                                                                                                                                              hypothetical protein A532L - Chlorella virus PBCV-1
C,Species: Chlorella virus PBCV-1
C,Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 2C477.6 - Caenorhabditis elegans
C.Spsciese: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: 127605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: EMBL:U42580; NID:94028896; PIDN:AAC96899.1
A,Experimental source: specific host Chlorella strain NC64A
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A;Description: The sequence of C. elegans cosmid ZC477.
A;Reference number: Z20392
A;Accession: T27605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 19; DB 2; I 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-79 <GRA>
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A;Molecule type: DNA
A;Residues: 1-79 <DUZ>
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R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T18034
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Best Local Similarity 100.v.
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Matches 4; Conservative
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A;Gene: CESP:ZC477.6
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Nacession: D97045

Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, in Dally, M.U.; Bennett, G.N.; Xoonin, E.V.; Smith, D.R.

Bacteriol. 183, 4833-4838, 2001

NTitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A.Reference number: A96900; MUID:21359325; PMID:21359325
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;Joate: Se.May-1993 #text_change 17-Mar-1999
;Joate: Se.May-1993 #text_change 17-Mar-1999
;Joate: Sol277; S25273
;Kalionis, B.; Dodd, I.B.; Egan, J.B.
;Malionis, B.; Dodd, I.B.; Egan, J.B.
;Malionis, Biol. 191, 199-209, 199-209, 198-209, 198-209, 198-209, 198-209, 198-209, 198-209, 198-209, 198-209, 198-209, 198-209, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-200, 198-20
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;Dibbens, J.A.; Gregory, S.L.; Egan, J.B.
Gol. Microbiol. 6, 2643-2650, 1992
;Title: Control of gene expression in the temperate coliphage 186. X. The cl repressor; Reference number: S25273; MUID:93078618; PMID:1447973
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4;Molecule type: DNA
4;Residues: 1-74 <KUR>
4;Cross-references: GB:AE001437; PIDN:AAK79151.1; PID:g15024100; GSPDB:GN00168
4;Experimental source: Clostridium acetobutylicum ATCC824
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A;Molecule type: DNA
A;Residues: 1-64 «KVI»
A;Cross-references: GB:L26909; NID:g598395; PIDN:AAC42221.1; PID:g598396
C;Genetics:
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                                                                                                                                                                                      A;Introns: 14/1
C;Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 19; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 4; Conservat
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Residues: 1-75 <KAL>
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Residues: 1-75 <DIB>
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                                                                                                                                             A;Gene: Tf
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;Gene: BH2182

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hypothetical protein ypjB [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C,Species: Lactococcus lactis Lactococcus lactis C,Species: Lactococcus lactis L, Mincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss; A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein Atu4039 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 11.7an-2002 #sequence_revision 11.7an-2002 #text_change 18-Nov-2002 C; Accession: AB3053 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelli Karp, P.; Romero, P.; Zhang, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Yerainia pestis
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C; Accession: T15018
C; Accession: T15018
R; Lindler, L.B.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A; Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid A; Reference number: Z18268; WID:99043898; PMID:9826348
A; Accession: T15018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE005176; PID:g12724551; PIDN:AAK05648.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                          Indels
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100.0%; Score 19; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0;
       100.0%; Pred. No. 2.5e+02; iive 0; Mismatches 0;
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          Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conserv
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                                                                                                                                                       12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 VAEF 71
                                                                                                          1 VAEF 4
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Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

Date: 20-Sep-1991 #sequence_revision 20-Sep-1991 #text_change 05-Dec-1997

Date: 138725

Tu, G.F.; Achen, M.G.; Aldred, A.R.; Southwell, B.R.; Schreiber, G.

Biol. Chem. 266, 6201-6208, 1991

Title: The distribution of cerebral expression of the transferrin gene is species speciate commer: A38725; MUID:91177867; PMID:1848850

Status: preliminary
Residues: 1-84 <STO>
;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05901.1; GSPDB:GN0d
;Experimental source: strain C-125
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Superfamily: Escherichia coli ribosomal protein S15; eubacterial ribosomal protein S15
23-89/Domain: eubacterial ribosomal protein S15 homology <ES15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ibosomal protein S15 - Haemophilus influenzae (strain Rd KW20)
Species: Haemophilus influenzae
Date: 10-Sep-1999 #text_change 10-Sep-1999
Accession: H64116; E64126
Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Stence 269, 496-512, 1995
Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
Accession: H64116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:U32812; GB:L42023; NID:91574784; PIDN:AAC22973.1; PID:91574788; Note: named as homolog to a protein from Escherichia coli Accession: E64125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: nucleic acid sequence not shown; translation not shown. Molecule type: DNA
Residues: 1-89 < ITGS.
Cross-references: GB.U32825; GB:L42023; NID:g1574307; PIDN:AAC23117.1; PID:g1574309; Note: named by homology to a protein from Escherichia coli
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Residues: 1-89 <TIG1>
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                                                                                                                                                                                                  Length 84;
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                                                                                                                                                                                                                                                                  0; Indels
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.Superfamily: transferrin; transferrin repeat homology
.Keywords: duplication
                                                                                                                                                                                              Query Match
100.0%; Score 19; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity
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Residues: 1-87 <TUA>
                                                                                                                                                                                                                                                                                                                                                                                             38 VAĖF 41
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Query Match

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Gaps

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C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 2-4-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: H59297
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffirles, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Farrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Reference number: Apyl39
A;Reference number: Apyl39
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Cispecies: Methanococcus maripaludis
Cipate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
Cipate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
Cipate: 20-Sep-1999 #sequence_revision 3.7. Leigh, J.A.
Bitcheriol 179, S41-543, 1997
A;Title: Nitrogenase phylogeny and the molybdenum dependence of nitrogen fixation in Met A;Reference number: 216944, MUID:97144542; PMID:8990309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AE006641; NID: 913814625; PIDN: AAK41639.1; GSPDB: GN00155
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A;Experimental source: strain JJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein [imported] - Sulfolobus solfataricus
                                                                                                                                                                      Length 99;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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C64490
hypothetical protein MJ1524 - Methanococcus jannaschii
                                                                                                                                                                 Query Match
100.0%; Score 19; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.8e+02;
ive 0; Mismatches 0;
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A, Experimental source: strain PAO1
C,Genetics:
A,Gene: PA3202
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-101 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                             62 VAEF 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Observed hypothetical protein Imo2579 [imported] - Listeria monocytogenee (strain EGD-e J.Species: Listeria monocytogenes
J.Species: Listeria monocytogenes
J.Species: Listeria monocytogenes
J.Baccession: AC1397
S.Accession: AC1397
S.Accession: AC1397
S.Accession: L. Backer, L.; Buckrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Dominguez-Bernal, G.; Soloteser, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.K. C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Joseff hypothetical protein PA3202 [imported] - Pseudomonas aeruginosa (strain PA01) [imported] - Pseudomonas aeruginosa [imported] - Pseudomonas aeruginosa [imported] - Pseudomonas aeruginosa [imported] - Imported] - Imported | Im
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4;Molecule type: DNA
4;Residues: 1-99 <STO>
4;Cross-references: GB:AE004744; GB:AE004091; NID:g9949317; PIDN:AAG06590.1; GSPDB:GN001
Science 294, 2317-2323, 2001
A,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                              ster, E.W.
Affille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3053
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4,Experimental source: strain EGD-e
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                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE008689; PIDN:AAL44840.1; PID:g17742484; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
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Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A, Molecule type: DNA
A, Residues: 1-96 < KUR>
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A;Molecule type: DNA
A;Residues: 1-97 <GLA>
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A; Experimental source: specific host Chlorella strain NC64
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C, Genetics:
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Cross-references: GB:AL021646; GB:AL123456; NID:g3242278; PIDN:CAA16648.1; PID:g282759
Experimental source: strain H37Rv
         parter 13.5ep-1996 #sequence_revision 13-Sep-1996 #text_change 12-Jun-2003
Accession: C64490
; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.J.; Worstee, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Sedow, P.W.; Hurst, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. cience 273, 1058-1073, 1996
; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G. Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii; Reference number: A64300; MulD:96337999; PMID:8688087
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Cole S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Jandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Authors: Squares, S.; Sulton, J.S.; Taylor, K.; Whitehead, S.; Barrell, B.G. Jaltle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome Reference number: A70500; MUID:98295987; PMID:9634230

Reference number: A70509

Reference number: A70509

Reference number: A70509

Reference number: A70509

Reference number: A70509
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                                                                                                                                                                                                                                                                                                                               Status: preliminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA
Residues: 1-108 <BUL>
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Date: 17-011-1998 #sequence_revision 17-0ul-1998 #text_change 20-Jun-2000
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$\text{Species: Chlorella virus PBCV-1}$
$\text{Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000}$
$\text{Accession: T17582}$
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;Residues: 1-111 <GRA>
;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96460.1
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;Superfamily: uncharacterized conserved protein MJ1524
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ibmitted to the EMBL Data Library, May 1999
;Reference number: 218806
Accession: 117882
      Species: Methanococcus jannaschii
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Best Local Similarity 100.
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Cjaccesion: B83431
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laxbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon A;Reference number: A82950; MUD:20437337; PMID:10984043
A;Accession: B83431
A;Accession: B83431
A;Accession: Drellminary
A;Accelled type: DNA
A;Residues: 1-112 < GTC>
A;Cross-references: GB:AE004598; GB:AE004091; NID:g9947687; PIDN:AAG05111.1; GSPDB:GN001
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R;Hofstead, S.J.; Matson, J.A.; Malacko, A.R.; Marquardt, H.
A. Antibiot. 45, 1250-1254, 1992
A;Fitle: Kedarcidin, a new chromoprotein antitumor antibiotic. II. Isolation, purification, A;Reference number: A55872; MUID:93015257; PMID:1399845
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submitted to the Brookhaven Protein Data Bank, June 1994
A;Reference number: A52519; PDB:1AKP
A;Contents: annocation; conformation and disulfide bond assignments by (1)H-NMR, residues
A;Contents: annocation; conformation and disulfide bond assignments by (1)H-NMR, residues
R;Zein, N.; Casazza, A.M.; Doyle, T.W.; Leet, J.E.; Schroeder, D.R.; Solomon, W.; Nadler,
Proc. Natl. Acad. Sci. U.S.A. 90, 8009-8012, 1993
A;Title: Selective proteolytic activity of the antitumor agent kedarcidin.
A;Reference number: A58601; MUID:93376732; PMID:8357457
A;Contents: annocation, protein activity
A;Note: the apported may have proteolytic activity
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A;Residues: 1-114 <-ROF>
A;Note: sequence extracted from NCBI backbone (NCBIP:118354)
R;Constantine, K.L.; Colson, K.L.; Wittekind, M.; Friedrichs, M.S.; Zein, N.; Tuttle, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: psc1; PA1722
C;Superfamily: Yersinia enterocolitica plasmid pYV virC-region hypothetical protein ysc1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type III export protein PscI PA1722 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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C.Species: Streptoalloteichus sp.
A.Yariety: strain LSB-6 (ATCC 53650)
C.Date: 21-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 15-Sep-2000
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                                                                                                                                                                      Length 111;
C,Genetics:
A,Gene: A92L
C,Superfamily: Chlorella virus PBCV-1 hypothetical protein A92L
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: P55327
C;Accession: P55327
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
; Xalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lypothetical protein SMa0974 [imported] - Sinorhizobium meliloti (strain 1021) magaplasm
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A;Experimental source: strain 1021, megaplasmid pSyma
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
                                       C,Accession: A01608
R;Hobart, P.M.; Shen, L.P.; Crawford, R.; Pictet, R.L.; Rutter, W.J.
Science 210, 1360-1363, 1980
A;Title: Comparison of the nucleic acid sequence of anglerfish and mammalian insulin mRJ
A;Reference number: A94254; MUID:81056434; PMID:7001633
                                                                                                                                                                                                                                                                                  A, Molecule type: mRNA
A, Residues: 1-116 < HOB>
C, Residues: 1-116 < HOB>
C, Residues: 1-116 < HOB>
A, Residues: 1-116 < HOB>
C, Residues: 1-116 < HOB </HOB 
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 16-Jul-1999
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R; Poustka, A.; Wellanreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, submitted to the Protein Sequence Database, April 2000
A; Reference number: 224535
A; Accession: 748682
A; Status: preliminary
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Similarity 100.0%; Score 19; DB 1; Length 116;
4; Conservative 0; Mismatches
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A;Residues: 1-118 cAAA-
A;Cross=references: EMBL:AL353932
A;Experimental source: adult amygdala; clone DKFZp761N05121
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Best Local Similarity
Matches 4; Conserv
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A;Note: DKFZp761N05121.1
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A;Molecule type: DNA
A;Residues: 1-119 <KUR>
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A, Rolecule type: DNA
A, Residues: 1-115 < KAW>
A, Cross-references: GB: AJ248283; GB: AL096836; NID: G5457433; PIDN: CAB49195.1; PID: e151508
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uypochetical protein AGR_C 804 [imported] - Agrobacterium tumefaciens (strain C58, Cered 5, Species: Agrobacterium tumefaciens 5, Species: Agrobacterium tumefaciens 5, Species: Agrobacterium tumefaciens 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 5, Accession: D97414 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 5, Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2322-2328, 2001 #the Plant Pathogen and Biotechnology Agent Agrobacterium tum 4; Reference number: A97359; MUID:21608551; PMID:11743194
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D15218
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Recession: D75218
A;Status: preliminary
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                                                                                                                                      Length 114;
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100.0%; Score 19; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                  Query Match 100.0%; Score 19; DB 2; I Best Local Similarity 100.0%; Pred. No. 3.2e+02; Matches 4; Conservative 0; Mismatches 0;
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             C;Keywords: antibiotic; pigment binding F;37-47,88-95/Disulfide bonds: #status experimental
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C;Species: Lophius americanus (American goosefish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: AGR C 804
A;Map position: circular chromosome
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4,Molecule type: DNA
4,Residues: 1-114 <KUR>
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Genetics

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A; Gene: PAB0185

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Wypotherical protein Rv3675 - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C,Species: Mycobacterium tuberculosis
C,Adresion: 10-011-1998 #sequence_revision 17-011-1998 #text_change 22-Oct-1999
C,Adresion: D0790
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandeam, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-544, 1998
A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Atthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Reference number: A70500; MUID: 98295987; PMID: 9614230
A,Reference number: A70500; MUID: 98295987; PMID: 9614230
A,Reference number: A70500; Muid: sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-125 <COL>
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Ashtre 403, 665-669, 200
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A; Reference number: A81250; MUID:20150912; PMID:10688204
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A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
            ki, S.; Church, G.M.; Daniels, C.J.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. Bacteriol. 179, 7135-7155-1155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct: A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: B69129
A;Accession: B69129
A;Accession: breliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-125 <MTH>
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: GB:AE000810; GB:AE000666; NID:g2621277; PIDN:AAB84740.1; PID:g262128:
A;Experimental source: strain Delta H
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: B81368
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Similarity 100.0%; Fred. No. 3.5e+02;
4; Conservative 0; Mismatches 0;
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C,Superfamily: 4-carboxymuconolactone decarboxylase
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A,Gene: Rv3675
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Molecule type: DNA

Rolecule type: R
ela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Caience 293, 668-672, 2001
;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, ebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; Titler The composite genome of the legume symbiont Sinorhizobium meliloti.
;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: F82861
;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequentature 406, 151-157, 2000
Title: The genome sequence of the plant pathogen Xylella fastidiosa.
Reference number: A82515; MIID:20365717; PMID:10910347
Note: for a complete list of authors see reference number A59328 below
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;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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Best Local Similarity 100...
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Ricrossman, M.W.; Hauft, S.M.; Gordon, J.I.
Goll Biol. 126, 1547-1564, 1994
A.Fittle: The mouse ileal lipid-binding protein gene: a model for studying axial patterni A;Reference number: A54797; WUID:94375529; PMID:8089185
A.Accession: A54797
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C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72348
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; MUID:99287316, PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable cathepsin B-like cysteine proteinase (BC 3.4.22.-) 715B16.17b - Arabidopsis tha
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A;Molecule type: DNA
A;Residues: 1-129 <STO>
A;Cross-references: EMBL:AF104919; NID:g3859590; PIDN:AAC72873.1; PID:g3859607
A;Experimental source: cultivar Columbia
                                                                                    ileal lipid-binding protein - mouse
Species: Mus musculus (house mouse)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Nov-1999
C;Accession: A54797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 26-Peb-1999 #sequence_revision 26-Feb-1999 #text_change 22-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Modecule type: mRNA
A;Residues: 1-128 <CRO>
A;Cross-references: GB:U00938; NID:g507143; PIDN:AAC27352.1; PID:g507144
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Similarity 100.0%; Score 19; DB 2; Length 129;
8;milarity 100.0%; Pred. No. 3.7e+02;
4; Conservative 0; Mismatches 0; Indels
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R,Stoneking, T.; Smith, R.
submitted to the EMBL Data Library, November 1998
A;Description: The sequence of A. thaliana T15B16.
A;Reference number: Z14488
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C, Keywords: cysteine proteinase; hydrolase
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A;Introns: 23/1; 81/3; 111/3
C;Superfamily: myelin P2 protein
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Best Local Similarity 10v..
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A;Note: T15B16.17b
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Best Local Similarity
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D72348
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; May, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: Aslo77; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Sajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Atalandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. A; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Reference number: A70500, MulD:98295987; PMID:9634230
A; Accession: D70799
A; Accession: D70799
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-127 < COL>
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Experimental source: strain H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                           /Species: Mycobacterium tuberculosis
.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Listeria innocua
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                                                              Length 126;
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                                                        100.0%; Score 19; DB 2; I
100.0%; Pred. No. 3.6e+02;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conserv
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4,Molecule type: DNA
4,Residues: 1-127 <GLA>
                                                                                                                                                                                                                                   83 VAEF 86
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                                                                                                                                                                           1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: D70799
A, Gene: Cj0939c
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Gene: lin2399
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conserved hypothetical protein YPO1120 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Date: 02-Nov-2001
C;Date: 03-Nov-2001
C;Dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: H75623
R;White, O.; Esten, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.; A.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma} S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                   R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Dana Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                               hypothetical protein alr1525 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-133 «KUR»
A;Cross-references: GB:AL590842; PIDN:CAC89963.1; PID:g15979187; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-132 - CKUR>
A;Residues: 1-132 GB:BA000019; PIDN:BAB77891.1; PID:G17135345; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Score 19; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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C;Superfamily: rbcX protein
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A;Molecule type: DNA
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81 VAEF
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Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 06-Jan-2003
Accession: G75208
Danitted to the EMBL Data Library, July 1999
Description: Pyrococcus abyasi genome sequence: insights into archaeal chromosome struy. Accession: G75208
Status: preliminary
Accession: G75208
Status: preliminary
Accession: G75208
Status: Data Library
Accession: G75208
Status: Data CARMA
Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49118.1; PID:g545762
Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Anabaena sp.
Species: Anabaena sp.
Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 13-Sep-1998
Jaccession: UQ2210
Latimer, F.W.; Soper, T.S.
ene 126, 85-92, 1993
JTLLE: Overproduction of Anabaena 7120 ribulose-bisphosphate carboxylase/oxygenase in Reference number: UQ2270; MUID:93231541; PMID:8472962
                                                                                                                   Residues: 17-130 <ARN>
Cross-references: GB:AE001739; GB:AE000512; NID:g4981176; PIDN:AAD35739.1; PID:g498117
Experimental source: strain MSB8
Genetimental source: strain MSB8
Genetimental source: strain MSB8
Superfamely: conserved hypothetical protein MJ0315
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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 19; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pothetical protein PAB2224 - Pyrococcus abyssi (strain Orsay)
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;Superfamily: uncharacterized conserved protein
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Residues: 1-132 <LAR>
Reserveferences: DDBJ:J01540
Reperimental source: strain 7120
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Accession: D72348
Status: preliminary
Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 VAEF 12
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-134 <BLAT>
A;Experimental source: GB:AB000177; GB:U00096; NID:g1786955; PIDN:AAC73830.1; PID:g1786957;
A;Experimental source: strain K-12, substrain MG1655
C;Comment: This is one of the proteins, encoded by the fii-tolAB gene cluster, that is is Genetics:
A;Gene: ybgC
A;Map position: 17 min
A;Start codon: GTG
C;Superfamily: 15.5K protein (tolAB operon 5' region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CiSpecies: Escherichia coli
CiSpecies: Escherichia coli
Escherichia coli
Escherichia coli
Escherichia coli
Escherichia coli
CiAccession: C90725
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishili, K.; Yokoyama, K.; Han, C.G.
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishili, K.; Yokoyama, K.; Han, C.G.
Byasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA, Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Tetle: Complete Genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Accession: C90725
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pothetical protein ECs0771 [imported] - Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross references: GB:BA000007; PIDN:BAB34194.1; PID:g13360230; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        th Similarity 100.0%; Score 19; DB 2; Length 134; Similarity 100.0%; Pred. No. 3.86+02; 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 19; DB 1; I
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: ECs0771
C;Superfamily: 15.5K protein (tolAB operon 5' region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: 15.5K protein (tolAB operon 5' region)
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A, Molecule type: DNA
A, Residues: 1-134 <STO>
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A; Residues: 1-134 <HAY>
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Matches
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Diate: 0.2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

Diate: 0.2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

Diacession: A84221

River M.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. River, M.V.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A.Athuhors: Hou, S.; Daniels, C.J.; Dennis, P.D.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A.Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ybgC protein - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 15-Oct-1982 #sequence_revision 30-Jun-1988 #text_change 01-Mar-2002
C;Accession: A25980; G64809
C;Accession: A25980; G64809
J; Bacteriol. 169, 2667-2674, 1987
A;Title: Nucleotide sequence of a gene cluster involved in entry of E colicins and singla A;Reference number: A91835; MJD:8722192; PMID:3294803
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A;Residues: 1-134 <SUN>
A;Cross-references: GB:M16489; NID:g148021; PIDN:AAA83918.1; PID:g1128977
A;Cross-references: GB:M16489; NID:g148021; PIDN:AAA83918.1; PID:g1128977
B;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                 A;Gross-references: GB.AE001826; NID:g6460827; PIDN:AAF12590.1; PID:g6460886; TIGR:DRB0C
A;Experimental source: strain R1
              Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.; Reference number: A75250; MUID:20036896; PMID:10567266
; Accession: H75623
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;Cross-references: GB:AB004437; NID:g10580221; PIDN:AAG19133.1; GSPDB:GN00138
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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4, Genome: plasmid
                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <WHI>
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                                                                                                                                                                                                                                                                                                                                 Gene: DRB0052
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A;Cross-references: GB:AE005174; NID:g12513669; PIDN:AAG55072.1; GSPDB:GN00145; UWGP:Z09
A;Experimental source: strain 0157:H7, substrain EDL933
Ypothetical protein ybgC [imported] - Escherichia coli (strain 0157:H7, substrain EDL93
                                                                                                                                                                                    D.J.; Mayhew
K.; Apodaca,
                                                            C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C; Accession: D85576
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
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C; Superfamily: hypothetical protein yneT
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Matches 4; Conserv
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A;Residues: 1-138 <HEI>
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Species: Synechocystis sp.
Accession: S76416
Seach S., Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
NA Res. 3, 109-136, 1996
Synechocystis
Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Silonocalla electrica subsp. electrica servoar Typhi Species: Salmonella enterica subsp. enterica in Species: Salmonella enterica subsp. enterica servoar Typhi Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 Pacession: AD0592 Pacession: AD0592 Packhill; J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, J.; T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; Jo'soara, P. ature 413, 848-852, 2001 Patric 413, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 848-852, 
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;Residues: 1-156 «KDA.)
;Cross-references: EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BAA18545.1; PID:g165363
;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                 onserved hypothetical protein STY0790 [imported] - Salmonella enterica subsp. enterica
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Nolecule type: DNA
Residues: 1-134 APAR>
(Cross-references: GB:ALS13382; PIDN:CAD05206.1; PID:g16501976; GSPDB:GN00176
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100.0%; Score 19; DB 2; Length 134; 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels
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Similarity 100.0%; Pred. No. 3.8e+02;
4; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 4; Conservative
                                     Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conserv
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        Query Match
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81355
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A69052

ribofiavin synthase beta subunit - Methanobacterium thermoautotrophicum (strain Delta H)

ribofiavin synthase beta subunit - Methanobacterium thermoautotrophicum

c;Species 16-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-May-2000

C;Accession: A69052

C;Accession: A69052

R; Simith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F

Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functs

A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: A69052
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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: B81355
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel.
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Reference number: A81250; MUID:20150912; PMID:10688204
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A.Experimental source: serogroup O1; strain N16961; biotype El Tor
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XResidues 1.137 cPAR.
A;Cross-references: GB:XL139076; GB:AL111168; NID:g6968128; PIDN:CAB73094.1; PID:g696827:
A;Experimental source: serotype 02, strain NCTC 11168
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ilarity 100.0%; Pred. No. 3.9e+02;
Conservative 0; Mismatches 0;
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100.0%; Score 19; DB 2; Best Local Similarity 100.0%; Pred. No. 3.9e+02; Matches 4; Conservative 0; Mismatches 0;
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Query Match Best Local Similarity 100.

',Status: preliminary
',Molecule type: DNA

1; Gene: BH2601 ;;Genetica:

., Accession: A83975

11 VAEF 14

1 VAEF 4

≿ ŏ 65 VAEF 68

1 VAEF 4

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riboflavin synthase, subunit beta (ribE) homolog - Archaeoglobus fulgidus c) Species: Archaeoglobus fulgidus () Species: Archaeoglobus fulgidus () Species: Archaeoglobus fulgidus () Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000 () Accession: H69515 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000 () Accession: H69515 #sequence_revision () F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson F.; Klank, H.P.; Charter 390, 364-370, 1997 #s.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997 #r.; Gotton, M.D.; Spriggs, T.; Artiach, D.; Kaine, B.P.; Sykes, S. Smith, H.O.; Nocse, C.R.; Venter, J.C. A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo A; Attereace number: A69250; MuID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            low-temperature regulated protein BN19 - rape
()Species: Brassica napus (rape)
()Species: Brassica napus (rape)
()Species: D.Sep-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
()Accession: 402280
()R.Weretinyk, E.; Orr, W.; White, T.C.; Iu, B.; Singh, J.
()R.Weretinyk, E.; Orr, W.; White, T.C.; Iu, B.; Singh, J.
()A.Title: Characterization of three related low-temperature-regulated cDNAs from winter B A;Reference number: 402279; MUD:94105287; PMID:7904076
A;Recession: 402280
A;Residues: 1-142 cWRRs
A;Residues: 1-142 cWRRs
A;Comment: This protein is a low-temperature-related protein.
                                                                                                                           Ow-temperature regulated protein BNI15 - rape
(Species: Brassica napus (rape)
(Species: Brassica napus (rape)
(Species: Brassica napus (rape)
(Species: 30-8p-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
(SAccession: 072279
(SAccession: 10, 171-17, 1993
(SAccession: Din, 171-17, 1993
(SAccession: 10, 171-17, 1993
(SAccession: 072279)
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C;Superfamily: riboflavin synthase beta chain
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100.0%; Score 19; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 46+02;
ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 4; Conservative
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";Species: Archaeoglobus fulgidus
";Species: Archaeoglobus fulgidus
";Species: Archaeoglobus fulgidus
";Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
";Accession: B69323
";Accession: B69323
";Accession: R.D.; Quackenbush, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
";Aleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.;
"; Pleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.;
"; Atture 390, 364-370, 1997
";Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
";Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
";Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
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4, Residues: 1-140 «KLB»
1, Cross-references: GB: AE001064; GB: AE000782; NID: 92689387; PIDN: AAB90658.1; PID: 9265004
2, Superfamily: Archaeoglobus fulgidus hypothetical protein AF0586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jrakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiralucleic Acids Res. 28, 4317-4331, 2000
Ucleic Acids Res. 28, 4317-4331, 2000
Jritle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and Jreference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iResidues: 1-139 <STO>
)Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06320.1; GSPDB:GN00
; Experimental source: strain C-125
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1, Status: preliminary; nucleic acid sequence not shown; translation not shown
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| Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
| A83975
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100.0%; Score 19; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.9e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0.
                                                                                                                                                    , Gene: MTH1390
.; Superfamily: riboflavin synthase beta chain
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DNA Res. 3, 109-136, 1996
A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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Variety: PCC 6803
Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
Accession: 877043
S. Accession: 877043
Xancession: 87.5 Asto, 8.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:AL109949; PIDN:CAB52892.1; GSPDB:GN00070; SCOEDB:SCJ11.07c
Experimental source: strain A3(2)
Comment: A complete transposase sequence can be assembled from three adjacent orfs (PI
                                                                                                                                                                                                                                                                                                        obable transposase, truncated section 1 [imported] - Streptomyces coelicolor (fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: B41715
; Kroemer, W. J. , Arndy. E. .
. Biol. Chem. 266, 24579-24579, 1991
;Title: Halobacterial S9 operon. Three ribosomal protein genes are cotranscribed with
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;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
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|Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 14-Apr-2003
                                                             Gabs
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Cross-references: GB:M76567; NID:g148775; PIDN:AAA73097.1; PID:g148777
Superfamily: ribosomal protein L13
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     Length 143;
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  100.0%; Score 19; DB 2; I
100.0%; Pred. No. 4.1e+02;
cive 0; Mismatches 0;
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Molecule type: DNA
Residues: 1-143 <OLI>
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Best Local Similarity 100.
Matches 4; Conservative
     Query Match 100.
Best Local Similarity 100.
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Best Local Similarity
Matches 4; Conserv
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Cjacession: F98837
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Inoue, S.; Kiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Aceference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F89837
A;Molecule type: DNA
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C. Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon J. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
Apturbors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Little: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A, Reference number: S74322, MUID:97061201, FMID:8905231
A;Accession: S77043
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1.145 <KAN>
A;Residues: 1.145 <KAN>
A;Cross-references: EMBL:D64005, GB:AB001339; NID:g1001779; PIDN:BAA10735.1; PID:g100658
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein s110678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein SA0624 [imported] - Staphylococcus aureus (strain N315)
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: LNA
A;Molecule type: LNA
A;Molecule type: NNA
A;Mosidues: 1-147 <STO>
A;Cross-references: GB:AE004437; NID:g10580903; PIDN:AAG19719.1; GSPDB:GN00138
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A;Cross-references: GB:BA000018; PID:g13700560; PIDN:BAB41857.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
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C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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100.0%; Score 19; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Score 19; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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us-09-594-978a-2.rpr

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124 VAEF 127
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Best Local S
Matches 4
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);Species: Neisseria meningitidis
);Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
);Accession: E81788
(;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, M;Reference number: Agric 200-506, 2000
);Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
);Accession: E81788
);Accession: E81788
);Accession: E81788
);Accession: E81789
);Accession: E81789
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1,Residues: 1-148 <PAR>
1,Cross-references: GB:AL162758, GB:AL157959; NID:97380672; FIDN:CAB85372.1; FID:9738078
1,Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                        "ypothetical protein SC2E1.35 - Streptomyces coelicolor
'Species: Streptomyces coelicolor
'Species: Streptomyces coelicolor
'Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 04-Mar-2000
'Accession: T34803
'Natphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
'Naterence number: Z21557
'NAccession: T34803
'Accession: T34803
'Accession: T34803
'Accession: T34803
'Accession: T34803
'Molecule type: DNA
'Nolecule type: DNA
'Nolecule type: DNA
'Nolecule type: DNA
'Cross-references: EMBL:AL023797; PIDN:CAA19410.1; GSPDB:GN00070; SCOEDB:SC2E1.35
'Experimental source: strain A3(2)
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2.Species: Pyrococcus woesei
2.Spate: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993
3.Accession: 810655
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',Superfamily: Streptomyces coelicolor hypothetical protein SC2E1.35
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Query Match 100.0%; Score 19; DB 2; Length 147; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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?;Superfamily: hypothetical protein ytwl
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Gypeudoazurin [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
Cyspecies: Agrobacterium tumefaciens
Cyspeciens
Cyspecies: Agrobacterium tumefaciens
Cyspeciens
Cysp
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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AC1137
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maritle: Comparative genomics of Listeria species
A;Reference number: AB1077; MUD:21537279; PMID:11679669
R;Zwickl, P.; Fabry, S.; Bogedain, C.; Haas, A.; Hensel, R.
J. Bacteriol. 172, 4329-4338, 1990
J. Bacteriol. 172, 4329-4338, 1990
Shithle: Glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaebacte scherichia coli.
A;Reference number: S10650; MUID:90330536; PMID:2165475
A;Accession: S10655
A;Molecule type: DNA
A;Residues: 1-148 < CMI>
A;Note: the authors translated the codon GGT for residue 54 as Glu
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A;Status; parilininary
A;Nolecule type: DNA
A;Residues: 1-149 <GLA>
A;Creas references: GB:NC_003210; PIDN:CAC98577.1; PID:g16409874; GSPDB:GN00177
A;Creas references: Gtrain EGD-e
C;Genetics:
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, Molecule type: DNA
, Readdues: 1-150 «KUNA.
, Cross-references: GB:AE008688; PIDN:AAL43272.1; PID:g17740759; GSPDB:GN00186
, Experimental source: strain C58 (Dupont)
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Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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:Gene: Atu2283

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Search completed: May 24, 2004, 17:38:37
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Best Local Similarity 100.
Matches 4; Conservative
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Cross-references: GB.NC_003210; PIDN:CAC98328.1; PID:g16409472; GSPDB:GN00177
Experimental source: strain EGD-e
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Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Accession: AB1089
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                                                                                                Length 150;
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100.0%; Pred. No. 4.3e+02;
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Q8zyd8 pyrobaculum P42590 escherichia P19487 xanthomonas P21885 bacillus su O52351 mycoplasma P57693 thermoplasma P57693 thermoplasma P576288 arabidopsis Q8572 anabacha sp O4651 drosophila P72245 rhodobacter P40051 saccharomyc Q22412 rickettsia Q9aby4 c bifunctic P26334 trypanosoma P88140 saccharomyc P49109 cavia pomce P405109 cavia parcializational page P405109 cavia pomce P40510		Actinomycetales; cerium.	F C.ELEGANS P20A1.4 Fin in the translation of CRC64;	1; Length 19; 0; Indels 0; Gaps 0;		AA. date) date) Spirochaetaceae; Treponema.
SYC_PYRAE YGJT_ECOLI GUNA, XANCP DCLY_BACSU SECY_MYCGA SECY_MYCGA GALC_CAREL NU4C_ARATH YEQG_YEAST YEQG_YEQG_YEQG_YEQG_YEQG_YEQG_YEQG_YEQG_	IGNMENTS	DARD; 9, Created) 8, Last sequence update) 10, Last senotation update) 10, Last sequence. 11, Last sequence. 12, Last sequence. 13, Actinomacteridae, Actinomacteria; Actinomacteriae. Mycobacteriaceae; Mycobacterium.	iss-Prot. THE N-TERMINALS OF C To find this protein 37Rv.	%; Score 19; DB %; Pred. No. 35; 0; Mismatches		PRT; 59 sd) advence upda annoration up subunit. cochaetales;
24 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		TAD TO 43 C 433 C	apurna P.S 997) to Sw STRONG, TO NZAE H1096 are unable f strain H	100.0 arity 100.0 onservative) 등 4 1 - 1 - 4	STANDARD; 1. 37, Cr 1. 47, La 1. 47, La slocase s slocase s; chaetes; chaetes; Aa.
9 9 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	RESULT 1 NS2_MYCTU	ALL MAY COLL - JUL	RN SEQUENCE. RP SEQUENCE. RA PRESENTALISHED RICK, AN REL SUBMILTED (DEC. 1- SIMILARITY CC. 1- CAUTION: WALLED RICK CC. 1- CAUTION: WALLED RICK CO. 1- CAUTION: WALLED RICK	Ouery Match Best Local Simil: Matches 4; Co	Oy 1 VAEF Db 11 VAEF	SECE_TREPA SECE_TREPA SECE_TREPA SECE_TREPA SECE_1998 (Red) IS-DEC-1998 IS-DEC-1998

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STRAINSVC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.P., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                           Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.;

"Complete genome sequence of Treponema pallidum, the syphilis spirochete."

Science 281:375-386(1998).

-I- PUNCTION: Essential for protein export.

-I- SUBCELLULAR LOCATION: Tail-anchored membrane protein (Potential).

-I- SUBCELLULAR LOCATION: Tail-anchored membrane family.
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Södergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
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InterProj IPR001901, SecE.
InterProj IPR001807, SecE.
TIGRPAM, PF00584, SecE; 1.
TIGRPAM, TIGR00964, 3a0501806; 1.
PROSITE; PS01067; SECE SEC61G; 1.
Protein transport; Translocation; Transmembrane; Complete proteome.
TRANSMEM 39 59 POFENTIAL.
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Nature 390:364-370(1997)
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Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
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59 AA; 6789 MW; 9AC35BA8F48B2A7F CRC64;
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16-CCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical UPF0165 protein AF1090.
AF1090.
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029175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=727;
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P44389;
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                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDINTRE-95550630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Pritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Wenter J.C.,
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01.NOV-1995 (Rel. 32, Last sequence update)
01.NOV-1995 (Rel. 32, Last sequence update)
28.FBB-2003 (Rel. 41, Last annotation update)
Hypothetical protein HI0451.
Hamophilus influenzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
NCBI_TAXID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 19; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6887 MW; B72E847382B2B6B6 CRC64;
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TITR, H10451; --
Hypothetical protein; Complete proteome.
SEQUENCE. 63 AA; 7047 MW; 36B14E60AC306B67 CRC64;
SIMILARITY: Belongs to the UPF0165 family.
                                                                                                                                                                                                                                                                                                                                                PIR, A69386; A69386.

TIGR, AF1090;
Interpro, IPR008203; DUF104.
Interpro; IPR008204; DUF104.
ProDom, PD005964; DUF104.
Hypothetical protein; Complete pr SEQUENCE 59 AA; 6887 MW; B72E
                                                                                                                                                                                                                                                                                               EMBL; AE001028; AAB90157.1; -.
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Science 269:496-512(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95350630; PubMed=7542800; Patch State C., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., McKenlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Sortt J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Pritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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-!- FUNCTION: This protein is one of the 16S ribosomal RNA binding proteins (By similarity).
-!- SIMILARITY: Belongs to the S15P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
30S ribosomal protein S1s.
(RPSO-A OR RPSI5-A OR HI1328) AND (RPSO-B OR RPSI5-B OR HI1468)
Haemophilus influenzae.
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Pasteurellaceae; Haemophilus.
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100.0%; Score 19; DB 1; Length 63 ilarity 100.0%; Pred. No. 1.1e+02; Conservative 0; Mismatches 0; Indels
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PROSSITE; PS00362; RIBDSOMAL S15; 1.
Ribosomal protein; RRNA-binding; Complete proteome.
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                      88 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro: IPR00289; Ribosomal_815.
Interpro: IPR06289; Ribosomal_815_b.
Pfam; PF00312; Ribosomal_815, I.
ProDom; PD157043; RS15_bact; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 AA; 10064 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 VAEF 14
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ALB2_METKA

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0; Mismatches
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MEDLINE=93015257; PubMed=1399845;
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                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
  Methanococcus jannaschii.
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                                                                           NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VAEF 4
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RA Sleazev A.I., Mezhevapa K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozyavkin S.A.
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
C. I- FUNCTION: Binds double-stranded DNA tightly but without sequence
chromosome, suggesting a role in chromatin archites is therefore
chromosome, suggesting a role in chromatin by similarity.
C. I- SUBINIT: Homoterramer (By similarity).
C. I- SUBINIT: Homoterramer (By similarity).
C. I- SUBINITY: Belongs to the archeoby repressing transcription. Regulation of DNA-based activities is therefore
achieved at the chromatin level (By similarity).
C. I- SIMILARITY: Belongs to the archeapal histone-like Alba family.
C. I- SIMILARITY: Belongs to the archeapal histone-like Alba family.
C. I- SIMILARITY: Belongs to the archeapal histone-like Alba content is in no way the European Bioinformatics Institutes. There are no restrictions on its Couse by non-profit institutions as long as its content is in no way condities requires a license agreement (see http://www.isb-sib.ch/announce/correct or send an email to license@ieb-sib.ch).
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                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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InterPro; IPR002775; DUF78.
Pram, PR01918; DUF78; 1.
ProDom; PD010497; DUF78; 1.
TIGRFAMS; TIGR00285; TIGR00285; 1.
DNA-binding; Acetylation; Complete proteome.
ACETYLATION (BY SIMILARITY).
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                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA-binding protein Alba 2.
Methanopyrus kandleri.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ1524.
MJ1524.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE010398; AAM02302.1; -.
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4; Conservative 0
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                                                                                               STANDARD;
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Best Local Similarity
Matches 4; Conserv
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Q58919;
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Q8TWE6;
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YF24_METJA RESULT 7

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                                                                                                                                                                                                                                                                            STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

XI MEDLINE=96337999; PubMeda8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Railarge A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Raich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Puhrmann J.L., Nguyen D.,

A Cott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Cott J.L., Roberts K.M., Peterson J.D., Sadow P.W., Hanna M.C.,

A Cotton M.D., Roberts K.M., Smith H.O., Wese C.R., Venter J.C.,

KINK H.-P., Fraser C.M., Smith H.O., Wese C.R., Venter J.C.,

A complete genome sequence of the methanogenic archaeon, Methanococcus

Timnschii.", Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoferead S.J., Matson J.A., Malacko A.R., Marquardt H.; Isolation, "Kedarcidin, a new chromoprotein antitumor antiblotic. II. Isolation, purification and physico-chemical properties."; J. Antiblot. 45:1250-1224 (1992).
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Sslomon W., Nadler S.G.;
Sslemon W., Proteolytic G. 1
Fall Selective proteolytic G. 1
Fall Acad. Sci. U.S.A. 90:8009-8012(1993).
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales.
NCBI_TaxID=38989;
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Pfam: PR02641; DUF190; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 108 AA; 12398 MW; D3E286AFB9D4AF8B CRC64;
Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
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100.0%; Pred. No. 1.9e+02;
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KEDA ACTSL STANDARD; PRT; 114 AA.

AC P41249;
DT 01-FEB-1995 (Rel. 31, Created)

DT -FEB-1995 (Rel. 31, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
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SEQUENCE FROM N.A.
Andoh T., Nagasawa
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P01341;
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SEQUENCE
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Best Local
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                                                                                                                    -i- DOMAIN: THIS PROTEIN CONSISTS OF AN IMMUNOGLOBULIN-LIKE SEVEN-
STRANDED ANTI-PRALLEL BETA-BARREL DOMAIN LINKED TO A SUBDOWAIN
COMPOSED OF TWO BETA-HAIRPIN RIBBONS.
-i- SIMILARITY: Belongs to the neocarzinostatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Taleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes, Pleuronectoidei, Pleuronectidae, Verssper.
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114
10969 MW; 1901E2B14E4197B4 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pleuronectoide; Pleuronectidae; Verasper NCBL_TaxID=98923;
                                                                                                                                                                                    Antibiotic, DNA-binding, 3D-structure DISULFID 37
                                                                                                                                                    PDB, 1AKP, 31-AUG-94.
InterPro; IPR002186; Neocarzinostat.
Pfan, PF00960; Neocarzinostat, 1.
ProDom; PD012709; Neocarzinostat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Verasper moseri (Barfin flounder).
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.000
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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112
114 AA;
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Andoh T., Nagasawa H.;
"Two molecular forms of insulin from barfin flounder, Verasper moseri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MEDLINE=81056434; PubMed=7001633;
Hobart P.M., Shen L.-P., Crawford R., Pictet R.L., Rutter W.J.;
"Comparison of the nucleic acid sequence of anglerfish and mammalian insulin mRNA's from cloned cDNA's.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lophius piscatorius (Allmouth goosefish) (Anglerfish), and Lophius americanus (American goosefish) (Anglerfish). Bustaryota Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi; Actinopterygli; Neopterygli; Teleostei; Suteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygli; Lophilformes; Lophildae; Lophius.
                                                 are derived from a single gene.";
2001. Sci. 15:931-937(1998)
-!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.
-!- SUBUNIT: Reterodimer of a B chain and an A chain linked by two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 2e+02;
Mismatches 0; Indels
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INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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HSSP; P01315; IMPJ;
InterPro; IPR00482; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
PRINTS; PR00277; INSULINB.
SMRRT; SM0078; INSP; 1.
PROSITE: PS00262; INSULIN; 1.
INSULIN family; Hormone; Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the insulin family.
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C PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12608 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE OF 25-54 AND 96-116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 210:1360-1363(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
56
95
32
1
44
100
115 AA;
                                                                                                                                                                                                                                                              disulfide bonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insulin precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 VAEF 82
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GTR2_PIG

ID GTR2_PIG STANDARD;

AC 065786;

DT 28-FRB-2003 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VAEF 4
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                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                                 piscatorius).";
Hoppe-Seyler's Z. Physiol. Chem. 350:1286-1288 (1969).
-!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.
-!- SUBCNIT: Heterodimer of a B chain and an A chain linked by two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
              MEDLINE=70036620, PubMed=5389298;
Neumann P.A., Koldenhof M., Humbel R.E.;
"Amino acid sequence of insulin from the angler fish (Lophius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 1; Length 116; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 AA; 12737 MW; C686F8EF8183BEFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      EMBL, V00634; CAA23907.1; -.
PIR; A01608; IPAF.
INCSSP; P01308; 1LBH.
INCESP-0: 1PR004825; INB/IGF/relax.
Pfam; PF00049; InBulin; 1.
PRINTS; PR00277; INSULINB.
SMART; SM00078; INSULINB.
PROSTIF: PS00262; INSULIN; 1.
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OUGTO DROME

TO 0908F3;

TO 0908F3;

TO 0007-2003 (Rel. 42, Created)

TO 0007-2003 (Rel. 42, Last sequence update)

DT 10-007-2003 (Rel. 42, Last annotation update)

CG 14505.

CG 14505.

CG 14505.

CG DAGGET STANDARDA Arthropoda; Hexapoda; Insection of Consophila melanogaster (Fruit fly).

CG Neoplera; Bndoplerygota; Diptera; Brachycera; Muc Ephydroidea; Drosophila.

CG Neoplera; Bndoplerygota; Diptera; Brachycera; Muc Ephydroidea; Drosophila.

CG Neoplera; Bndoplerygota; Diptera; Brachycera; Mu (I)

RR MEDLINE-20196066; Pubmed=10731132;

RA Admantides P. G., Scherer S.E., Li P. W., Hoskins IRA Admantides P. G., Scherer S.E., Li P. W., Hoskins IRA George R.A., Lewis S.E., Richards S., Ashburner RA Sutton G.G., Wortman U.R., Yandell M.D., Zhang OR RA Standon R.C., Rogers Y.-H.C., Blazej R.G., Champe
                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the insulin family.
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C PEPTIDE.
INSULIN A CHAIN.
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INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
 SPECIES=L.piscatorius;
                                                                                                                                                                                     disulfide bonds.
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DISULFID
DISULFID
SEQUENCE
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RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Rabill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Baura A., Baxendale J., Baradatari D., Bolshakov S., Beeson K.Y., Benos P.V., Berman B.P., Bhadatari D., Bolshakov S., R. Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P., Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I., Bodson K. Downes M. Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Borbon K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferriera S., Fleischmann M., Boslen D., Hougher M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Ghuan P., Harris M., Harvey D.A., Heiman T.J., Well M., H., Ibegwam C., Alali M., Kalush F., Karpen G.H., Kz., Kenlison J.A., Ketchum K.A., Jasko P., Lei Y., Kevitsky A.A., Li Z., Kennison J.A., Ketchum K.A., Lasko P., Lei Y., Levitsky A.A., Li J. J.H., Li Elegwam C., Lasko P., Lei Y., Levitsky A.A., Li J. J., Morpherson D., Lasko, D., Lei Y., Levitsky A.A., Li J. J., Morpherson D., Markel B., McIntosh T.C., McLeod M.P., McDherson D., Ra Alazin G., Malshina N.V., Morbhy D.M., Nelson K.A., Nixon K., Nusskern D.R., Palazolo M., Pittuan G.S., Pan S., Pollard J., Puri V., Reese M.G., Rabuson M., Sturpski M.P., Smith T., Shipen E., Spradling A.C., Stapleron M., Skurpski M.P., Smith H., Svirekas R., Tector C., Turner R., Vanner S., Wang A.H., Wang X., Hang Z.-Y., Wassarman D.A., Weinstond G., Zhang S., Yao Q.A., Hang S., Phan S., Chang S.,
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"A Drosophila full-length CDNA resource.";
Genome B.Ol. 3:RSSEARCHGO80.1-RESEARCHGO80.8(2002).
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100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0;
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MEDLINE=22426066; PubMed=12537569;
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EMBL; AY084100; AAL89838.1; -.
FlyBaae; FBGN0034327; CG14505.
InterPro; IPR007967; DUF727.
Pfam; PF03303; DUF727; 1.
SEQUENCE 119 AA; 13534 MW; 83
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PASMU
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09CM<u>Y</u>0;
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Y670 PASMU
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                                                                                                                                                    Canty J.M., Young R.F., Fallavollita J.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

-!-FUNCTION: Facilitative glucose transporter. This isoform likely mediates the bidirectional transfer of glucose across the plasma membrane of hepatocytes and is responsible for uptake of glucose by the beta cells; may comprise part of the glucose-sensing mechanism of the beta cell. May also participate with the Na(+)/glucose cotransporter in the transcellular transport of glucose in the small intestine and kidney (By similarity).

-!-SUBCELULAR LOCATION: Integral membrane protein.

-!-SIMILARITY: Belongs to the sugar transporter family. Glucose transporter subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
28-FEB-2003 (Rel. 41, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member 2
(Glucose transporter type 2, liver) (Fragment).
Suc2A2 OR GLUT2.
Sus scrofa (Fig)
Sus scrofa (Fig)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 1; Length 120; 100.0%; Pred, No. 2.1e+02; ive 0; Mismatches 0; Indels
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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InterPro; IPR005829; Sub_transporter.
InterPro; IPR003629; Sug_transporter.
InterPro; IPR003639; Sug_transpt.
Pfam; PP00083; Sugar_transpt.
PRNINTS; PR00171; SUGAR_TRNSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT_1; PARTIAL.
PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L18e.
RPL18E OR PAE0672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF054835; AAC12737.1; -.
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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106 1
120 1
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SEQUENCE FROM N.A.
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                                                                                                                NCBI_TaxID=9823;
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Q8ZYQ2;
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TRANSMEM
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SEQUENCE
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18E PYRAE
    FEBBZGCCXZA41CC
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                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=IM2 / ATCC 51768 / DSM 7523;

MEDLINE=21664397; PubMed=11792869;

Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
-!- SIMILARITY: Belongs to the L18E family of ribosomal proteins.
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Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 1; Length 122; 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF_00329; -; 1.
InterPro; IPR001196; Ribosomal_L15.
InterPro; IPR000139; Ribosomal_L18e.
Pfam: PF00256; L15; 1.
PROSTIFE; PS01106; RIBOSOMAL_L18E, RALSE_NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 122 AA; 13252 MW; 88F3DB732C4E0394 CRC64;
ryropaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein PM0670 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AA.
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PIRSF; PIRSF000029; Cytochrome_D562; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Pm70;
MEDLINE=21145866; Pubmed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE009779; AAL62941.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                 aerophilum.";
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130 AA.

PRT;

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE-99287316; PubMed=10360571;

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Redicalberg J., Sutton G.G., Fleischmann R.D., Elsen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,

"Evidence for lateral gene transfer between Archaea and Bacteria from

Toponem sequence of Thermotoga maritima.";

Nature 399:333-328(1999).

-I-FUNCTION: Decarboxylation of S-adenosylmethionine provides the

aminopropyl modety required for spermidine biosynthesis from

putrescine (By similarity) required for spermidine biosynthesis from

putrescine (By similarity) methylsulfonnium salt + CO(2).

-I-CATALYTIC ACTYVITY: S-adenosyl-L-methionium salt + CO(2).

-I-CATALYTIC Belongs to the prokaryotic AdoMetDC family Subfamily
                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
5-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
(SamDC) (Contains: S-adenosylmethionine decarboxylase beta chain; S-adenosylmethionine decarboxylase alpha chain).
                                                                                                                                                                                                                                                                                                                         Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                     Q9WZC3;
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIGR; TM0655
                                                                              THEMA
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                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@labsab.ch).
                                                                                                                                                                                                                ö
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=DBA/2J; TISSUE-Liver;
MEDLINE=94375529; PubMed=8089185;
Crossman M.W., Hauft S.M., Gordon J.I.;
Crossman M.W., Hauft S.M., Gordon J.I.;
The mouse ileal lipid-binding protein gene: a model for studying axial patterning during gut morphogenesis.";
J. Cell Biol. 126:1547-1564 (1994).

-i. FUNCTION: ILEAL PROTEIN WHICH STIMULATES GASTRIC ACID AND PEPSINOGEN SECRETION. SEEMS TO BE ABLE TO BIND TO BILE SALTS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCEL_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BILIRUBINS.
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: Belongs to the fatty-acid binding protein (FABP)
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                                                                                                                                                 100.0%; Score 19; DB 1; Length 124; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0; Indels
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PROSITE; PS00214; FABP; 1.

Transport; Lipid-binding; Acetylation.

INIT WET 0 BY SIMILARITY.

I ACETYLATION (BY SIMILARITY).

1 ACETYLATION (BY SIMILARITY).
                                              1 23 POTENTIAL.
24 124 HYPOTHETICAL PROTEIN PM0670.
124 AA; 13746 MW; D7B2B468C7B51B9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Gastrotropin (GT) (lleal lipid-binding protein) (ILBP).
FABPE OR ILLEP.
Mus musculus (Mouse).
Hypothetical protein; Signal; Complete proteome.
SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 AA.
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InterPro; IPR000566; Lipocin cytFABP.
FEm.; PR00061; lipocalin; 1.
PRINTS; PR00178; FATTYACIDBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U00938; AAC27352.1; -. PIR; A54797; A54797.
                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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MGD; MGI:96565; Fabp6.
                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                   45 VAEF 48
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P51162;
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                                                                                               SEQUENCE
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN (BY SIMILARITY).
S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                 S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                       HAMAP; WF 00464; -; 1.
InterPro; IPR003876; SAWDC.
Pfam; PP02675; AdoMetDC; 1.
Spermidine biosynthesis; Lyase; Decarboxylase; Zymogen; Pyruvate;
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CLEAVAGE (NOWHYDROLYTIC) (BY S
CONVERTED TO A PYRUYOYL GROUP
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 130;
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100.0%; Pred. No. 2.3e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                            EMBL; AE001739; AAD35739.1; -. PIR; D72348; D72348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 AA; 14785 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
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ID Y194_PYRAB
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Gaps

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VAEF 94 1 VAEF 4

Best Loc Matches

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Escherichia coli
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P08999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                       Archaea; Buryarchaeota; Thermococci; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERMS;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB--2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=GES / Orsay,
MEDLINE=22511545; PubMed=12622808;
MEDLINE=22511545; PubMed=12622808;
MEDLINE=22511545; PubMed=12622808;
MEDLINE=22511545; PubMed=12622808;
Mochen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte (Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.,
"An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.", 2003).

And. Microbiol. 47:1495-1512(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERM: PF03686; UPF0146; 1.

PIRSF; PIRSF016725; UCP016725; 1.

Probom; PD021130; UPF0146; 1.

Hypothetical protein; Complete proteome.

BEQUENCE 131 AA; 14629 MW, D13F378187F832C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                     16-0cT-2001 (Rel. 40, Created)
16-0cT-2001 (Rel. 40, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0146 protein PYRAS01940.
Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 AA.
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NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ248283; CAB49118.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF 00341; -; 1.
ThterPro; IPR005353; UPF0146.
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Best Local Similarity 100.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR: G75208; G75208
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VAEF 4
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(SB_HALN1
) RISB_HALN1
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Sun T.-P., Webster R.E.; "Nucleotide sequence of a gene cluster involved in entry of E colicins and single-stranded DNA of infecting filamentous bacteriophages into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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SPECIES-E.coli; STRAIN-K12 / MG1655;
SPECIES-E.coli; STRAIN-K12 / MG1655;
MEDLINE-9426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein ybgC.
YBGC OR B0736 OR C0815 OR Z0904 OR EC80771 OR SF0561 OR S0574.
Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 19; DB 1; Length 133; 100.0%; Pred. No. 2.40+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE005011; AAG19133.1; -.
PIR; A84221; A84221.
HSSP; O66529; HGX.
HAMAP: MF 00178; -; 1.
InterPro; TR002180; DMRL synthase.
ProDom; PD003664; DMRL synthase.
Prodom; PD003664; DMRL synthase; 1.
Riboflavin blosynthesis; Transferae; Complete proteome.
SEQUENCE 133 AA; 13719 MW; B9724DC24660D6CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli 06,
Escherichia coli 0157:H7, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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-!-SIMILARITY: BELOWGS TO THE 4-HYDROXYBENZOYL-COA THIOESTERASE PAMILY: STRONG, TO H. INPLUENZAE H10386. . 0 SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a; MEDINE=22590774; PubMed=12704152; MedinE=22590774; PubMed=12704152; Medin W., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling P. Mau B., Perna N.T., Payre S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.B., "Complete genome sequence and comparative genomics of Shigella Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter. 100.0%; Score 19; DB 1; Length 134; 100.0%; Pred. No. 2.4e+02; ive 0; Mismatches 0; Indels C44582B6EC3BE989 CRC64; 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (BC 2.5.1.9)
(Lumazine synthase) (Riboflavin synthase beta chain).
RIBH OR WIH1390. EMBL, DE0013; BAA35402.1; ...
EMBL, AR016757; AAN19288.1; ...
EMBL, AR016757; AAN19288.1; ...
EMBL, AR016253; BAA35402.1; ...
EMBL, AR016253; BAA34194.1; ...
EMBL, AR01686; AAA41398.1; ...
EMBL, AR01699; AAN42205.1; ...
EMBL, AR016979; AAN42205.1; ...
EMBL, AR016979; AAN42205.1; ...
ENBL, AR016979; AAN42205.1; ...
ENGL, AR016979; AAN42205.1; ...
ENGL, AR016979; AAN4206.1; ...
ENGL, AR016979; AAN4206.1; ...
ENGL, AR0110; YbgC.
InterPro; IPR008644; AHBCOA_thiostrae.
InterPro; IPR008643; Thioestr_supf.
FIGHR, FR03061; 4HBCOA_THIOSTRERSE; I. BY SIMILARITY Methanobacterium thermoautotrophicum. flexneri serotype 2a strain 2457T."; infect. Immun. 71:2775-2786(2003). DENTIFICATION BY MASS SPECTROMETRY 134 AA; 15562 MW; Hydrolase; Complete proteome. EMBL; M16489; AAA83918.1; -. EMBL; AE000177; AAC73830.1; -EMBL; D90713; BAA35402.1; -. Local Similarity 100. STANDARD; 129 VAEF 132 1 VAEF 4 SPECIES=E.coli; RISB METTH 027443; SECUENCE Query Match RISB_METTH Matches RESULT 20 OC SEE DATA SO ઠે 셤

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RISB ARCFU
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                                               MEDINE-98037514; PubMed=9371463;

MEDINE-98037514; PubMed=9371463;

MEDINE-98037514; PubMed=9371463;

Marcage T., Bashizzae6h R., Blakely D., Cook R., Gilbert K.,

Marrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,

Spadafora R., Vicare R., Warng Y., Wierzbowski J., Gibson R.,

Jawani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

McOmplete genome sequence of Methanobacterium thermoautorrophicum

GoltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7135-7155(1997).

J. Bacteriol. 179:7135-7135-7135(1997).

J. Bacteriol. 179:7135-7135-7136-7140000 and L.-J.4-dihydrohy-2-butanone-4-phosphate via 6.7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of F-amino-6-(1'-D)-ribityl-amino-1-phosphate via 6.7-dimethyl-8-lumazine (By similarity).

J. (1H, JH) -pyrimidinendione with L.J.4-dihydrohy-2-butanone-4-phosphate vielding 6.7-dimethyl-8-lumazine (By similarity).

J. CAPALYTYIC ACTIVITY: 2.6.7-dimethyl-8-lumazine (By similarity).

Liboflavin + 4-(1-D-ribitylamino-5-6-dihydroxypyrimidine.

J. SIMILARITY: Riboflavin biosynthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=VCL6 / DSM 4304 / ATCC 49558;
MEDIJNE-96104 / PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 1; Length 139; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riboflavin biosynthesis; Transferase; Complete proteome.
SEQUENCE 139 AA; 15464 MW; B640D8D12EE2A862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A69052; A69052.
HSSP; P11989; IRVU.
HAMAP, MF 00178; -; 1.
INTERPRO; IPR002180; DWRL synthase.
Pfam; PR00885; DWRL synthase; 1.
ProDom; P000364; DWRL synthase; 1.
TIGRFAMS; TIGR00114; rIDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaeoglobaceae, Archaeoglobus, NCBI_TaxID=2234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last St
Hypothetical protein AF0586.
AF0586.
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 NCBI_TaxID=187420
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16-OCT-2001
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586 ARCFU
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MIDDINIPS-960494313; Pubbed=9389475;

MEDLINES-960494313; Pubbed=9389475;

MEDLINES-960494313; Pubbed=9389475;

METALINES-960494313; Pubbed=9389475;

METACHOR M.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., McKenney K., Adams M.D., Loftus B.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reducing archaeon Archaeoglobus fulgidus.";

Nature 390:364-370(1997).

-!- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione and L.3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit
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16-0CT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
6.7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DWRL synthase)
6.7-dimethyl-8-ribityllumazine synthase beta chain).
RIBH OR RIBE OR AF2128.
Ketchum K.A., Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou Joverbeek K., Gocayne J.D., Weldman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Arriach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Masson T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the hyperthermophilic, sulphate-
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SEQUENCE 140 AA; 16175 MW; D3B1FE3A62A05901 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchãeota, Archaeoglobi; Archaeoglobales;
Archaeoglobaceae, Archaeoglobus.
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TIGR, AF0586; -
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Page 18

us-09-594-978a-2.rsp

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxiD=10090;
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CLM4 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
       2,4(14,3H)-pyrimidinedione with L.3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).
-!- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-0-tibityl)lumazine = riboflavin + 4-(1-0-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
-!- PATHAY: Riboflavin blosynthesis; last step.
-!- SIMILARITY: Belongs to the DWRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A resolution.";
Science 289:905-920(2000).
-!- SIMILARITY: Belongs to the L13P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 43049;
MEDLINE=20396344; PubMed=10937989;
Ban N., Nissen P., Hansen J., Moore P.B., Steitz T.A.;
"The complete atomic structure of the large ribosomal subunit at
catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. PubMed=1840597; MEDILINE=92105119; PubMed=1840597; Mromen W.J., Arndt E.; "Halobacterial S9 operon. Three ribosomal protein genes are corrangeribed with genes encoding a tRNR(Leu), the enclase, putative membrane protein in the archaebacterium Haloarcula (Halobacterium) marismortui.";
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 19; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0: Indela
                                                                                                                                                                                                                                                                                                                                                         Riboflavin biosynthesis, Transferase, Complete proteome.
SEQUENCE 143 AA; 15645 MW; BBA3141206905410 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haloarcula marismortui (Halobacterium marismortui).
Archaea, Euryarchaeota, Halobacteria, Halobacteriales;
Halobacteriaceae, Haloarcula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
50S ribosomal protein L13P (Hmal13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 266:24573-24579(1991)
                                                                                                                                                                                                                                                                                                               Pfam; PF00885; DWRL synthase; 1.
ProDom; PD003664; DWRL synthase; 1.
TIGRFAMS; TIGR00114; ribH; 1.
                                                                                                                                                                                                                                                    HSSP, P11998, TRVV.
TIGR, AP7128, -
HAWAP; MF 00178; -; 1.
InterPro; IPR002180; DWRL_synthase.
                                                                                                                                                                                                                            EMBL; AE000957; AAB89124.1; -. PIR; H69515; H69515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 VAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2238;
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P29198;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.

KAWAI TISSUB-Tonque;
KRANHE-21085660; PubMed=1021851;
KRANHE-21085660; PubMed=1021851;
KRAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
KAWAI J., Shinagawa H., Shibata K., Yomoh H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishii Y., Komoh H., Adachi J., Yukuda S.,
Arakawa T., Hara A., Phunishii Y., Komoh H., Adanhawa I.,
Adaca K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
Saito T., Okada T., Ashburnar M., Batalov S., Casawant T.,
Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
Kuchi P., Lewis S., Matsuo T., Nikaido I., Pesole G., Quackenbush J.,
Kuchi P., Lewis S., Matsuo M., Ano H., Baldarelli R., Barsh G.,
Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
Blake J., Bofielli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Nynshaw-Boris A., Yoshida K., Hasesgawa Y., Kawaji H., Kohtsuki S.,
Lyons P., Wanghia A., Yoshida K., Hasesgawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .i. FUNCTION: Implicated in the early stage of ectopic ossification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, B41715; B41715; PARATONIC, PIR, PIR, B41715; PIR, B41715; PDB; IRPR; 26-SEP-01.
PDB; IRSA; 19-JUL-02.
PDB; IRSA; 19-JUL-02.
PDB; IRSA; 19-JUL-02.
PDB; IRSA; 23-JUG-02.
PDB; IRSA; 23-JUG-02.
PDB; IMSO; 06-SEP-02.
PDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CILM4 MOUSE STANDARD; PRT; 148 AA. 09JMB3; OSCH21; CDD1E3; CDC1E3; CDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  EMBL; M76567; AAA73097.1; -.
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115 VAEF 118

-!- SIMILARITY: Contains 3 EF-hand calcium-binding domains

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus woesei.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zwickl P., Fabry S., Bogedain C., Haas A., Hensel R.,
"Glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic
archaebacterium Pyrococcus woesei: characterization of the enzyme,
cloning and sequencing of the gene, and expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                          EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
EF-HAND 3 (POTENTIAL).
E -> V (IN REF. 2; BAB22914).
M -> V (IN REF. 2; BAB22914).
M -> V (IN REF. 1; BAB22914).
VEN -> 1 (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 1; Length 148; 100.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in GAPDH 3'region (ORF X) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 AA; 15256 MW; 8C7E51A072DF5D50 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=DSM 3773;
MEDLINE=90330536; PubMed=2165475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 172:4329-4338(1990)
                                                                                                                                                                                                                   MGD; MGI:1931464; Calm4.
InterPro; IPR002048; EF-hand.
InterPro; IPR001125; Recoverin.
                                                                                                                                                                                                                                                                                PRINTS; PR00450; RECOVERIN.
ProDom; PD00012; EF-hand; 2.
SMART; SN00054; EF, 4.
PROSITE; PS00018; FF HAND; 3.
Calcium-binding; Repeat.
                                                                                                                                    EMBL, AB036744, BAA95412.1, --
EMBL, AK009956; BAB26608.1; --
EMBL, AK009664; BAB26425.1; --
EMBL, AK009664; BAB22914.1; --
HSSP, P02593; ICDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 AA; 16767 MW;
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                                                                                                                                                                                                                                                                   Pfam; PF00036; efhand; 4
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                                                                                                                                                                                                                                                                                                                                                                           104
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PIR, S10655, S10655,
Hypothetical protein,
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 VABF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus.
NCBI_TaxID=2262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VAEF 4
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CA_BIND
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002)

-Ir VINCTION: Riboflavin synthase is a bifunctional enzyme complex
-Ir VINCTION: Riboflavin synthase is a bifunctional enzyme complex
catalyzing the formation of riboflavin from 5-amino-6 (11'-D)
- ribity1-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-
butanone-4-phosphate via 6,7-dimethy1-8-lumazine. The beta subunit
catalyzes the condensation of 5-amino-6 (11'-D)-ribity1-
amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-
butanone-4-phosphate yielding 6,7-dimethy1-8-lumazine (By
similarity).
-I- CATALYTIC ACTIVITY: 2 6,7-dimethy1-8-(1-D-ribity1)lumazine =
riboflavin + 4-(1-D-ribity4mino)-5-amino-2,6-dihydroxypyrimidine.
-I- PATHWAY: Riboflavin biosynthesis; last step.
-I- SIMILARITY: Belongs to the DMRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (BC 2.5.1.9) (DWRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
RIBH OR PAE3296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=INAZ / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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TIGRPAMS; TIGR00114; TibH; 1.
Riboflavin biosynthesis; Transferase; Complete proteome.
SEQUENCE 150 AA; 16474 MW; 73751C1363A8ADBD CRC64;
                                                                                                                                                                                                                                                                               Pyrobaculum aerophilum.
Archaea, Crenarchaecta; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SODC_PRIGL STANDARD; PRT; 152 AA. p11418; 01-007-1999 (Rel. 12, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update)
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                            150
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InterPro; IPR002180; DMRL_synthase.
Pfam; PP00885; DMRL_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE009923; AAL64819.1; -.
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                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aerophilum.";
                            RISB PYRAE
Q8ZTE3;
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SODC_PRIGL
RISB_PYRAE
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HAEIN
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45555555555555555555555554444444888
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                                                                                                                                                                                                                                                                                           MEDLINE=89290032; PubMed=2500367;
Calabrese L., Polticelli F., O'Neill P., Galtieri A., Barra D.,
Calabrese L., Polticelli F., O'Neill P., Galtieri A., Barra D.,
Calabrese L., Polticelli F., O'Neill P., Galtieri A., Barra D.,
Calabrese L., Polticelli F., O'Neill P., Galtieri A., Barra D.,
Calabrese L., Polticelli F., O'Neill P., Galtieri C.,
Calabresi Lution of arginine for lysine 134 alters electrostatic
Calabratic Active site in shark Cu,Zn superoxide dismutase.";
FRES Lett. 250:49-52(1989).
Calls and which are toxic to biological systems.
Calls and calls a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0980B5;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (RC 2.5.1.9) (DWRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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STRAIN=ATCC 35092 / DSM 1617 / P2;

STRAIN=ATCC 35092 / DSM 1617 / P2;

STRAIN=21332265, PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Theixamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland I.,
                                 Prionace glauca (Blue shark).
Bukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Bukaryoca; Metazoa; Chordata; Caleomorphii; Galeomorphii; Galeoidea; Carcharhinidea;
Carcharhinidae; Prionace.
NCBL_TaxID=7815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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COPPER.
BY SIMILARITY.
; 661764223C5AE CRC64;
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COPPER AND ZINC.
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Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)
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Matches 4, Conserv
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                                                                                                                                                                                                                                                                              SEQUENCE
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RISB SULSO
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Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 987.835-7840(2001).

-!-FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-

ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-

butanome-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-

amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-

butanome-4-phosphate yielding 6,7-dimethyl-8-lumazine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylanino)-5-amino-2,6-dihydroxypyrimidine.
-1-PATHWAY: Riboflavin biosynthesis; last step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-88115138; PubMed=2828309; Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.; Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.; Coning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalton J. Bacteriol. 170:489-498 (1988).
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STRAIN=Rd / KW20 / ArCC 51907;
STRAIN=Rd / KW20 / ArCC 51907;
STRAIN=S95350630; PubMede7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-P., Dougherty B.A., Merrick J.M.,
Kockenney K., Sutton G., Firzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Outer membrane lipoprotein PCP precursor (15 kDa lipoprotein) (PAL cross-reacting lipoprotein).
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Pasteurellaceae, Haemophilus.
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Interpro; IRR002186; DMRL synthase.
Pfan; PF00885; DMRL synthase; 1.
ProDon; PD003664; DMRL synthase; 1.
IGROPHMS; TIGR00114; x1bH; 1.
Riboflavin biosynthesis; Transferase; Complete proteome.
SEQUENCE 17247 MM; ADFA9E6A2C723210 GRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 1; I 100.0%; Pred. No. 2.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Reoghagen N.S.M., Grehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Wenter J.C., "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Lat sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 44).
17-MAR-2004 (Sequence (Common dandelion).
18-MAR-2004 (Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
18-MAR-2004 (Magnoliophyta; eudicotyledons; core eudicots; asterids;
18-MAR-2004 (Magnoliophyta; eudicotyledons; core eudicots; asterids;
18-MAR-2004 (Magnoliophyta; eudicotyledons; Cichorioideae; Cichorieae;
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                                                                                                                                                                                                                                        Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Complete proteome; Palmitate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-palmitoyl cysteine.
S-diacylglycerol cysteine.
S-GLVAERVF - VAGRRVRI (IN REF. 1)
D7880327FCF0C985 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OUTER MEMBRANE LIPOPROTEIN PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 1; Length 155; 100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the BetVI family.
                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLYB AND TO Y.ENTEROCOLITICA PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 157 AA.
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19 19 N-F
13 19 8-6
135 13 CSI
155 AA; 15425 MW; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, M18877; AAA24938.1; -. ERMBL, 032832; AAC23228.1; -. PIR; 164130; 164130.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 VAEF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=50225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Root;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAP TAROF
049065;
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                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";

DNA Res. 8:123-140(2001).

-!- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21456156; PubMed=11572479; Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahi S., Sekine M., Baba S.-I., Ankai A., Kosuqi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = ribollavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine-
-!- PATHWAY: Riboflavin biosynthesis; last step.
-!- SIMILARITY: Belongs to the DWRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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0
                                                                                                                                                                                                 100.0%; Score 19; DB 1; Length 157; 100.0%; Pred. No. 2.8e+02;
                                                                                                                                                                                                                                         0; Indels
                                                                      PERMY PF00407; Bet V I; I.

PRINTS; PR00634; BETALLERGEN.
PROSTITE; PS00451; PATHOGBNESI BETVI; 1.
Allergen; Plant defense; Pathogenesis-related protein.
SEQUENCE 157 AA; 17040 MW; 5892AB8593ABA7E0 CRC64;
                                                                                                                                                                                                                                         0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP; MF_00178; -; 1.
InterPro; IPRO0218; DMRL_synthase.
InterPro; DMRL_synthase; 1.
ProDom; PD003664; DMRL_synthase; 1.
TIGRFAMS; TIGR00114; rIbH; 1.
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                 EMBL; AF036931; AAB92255.1; -
HSSP; O24248; 1E09.
InterPro; IPR000916; Bet v.I.
                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-JCM 10545 / 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sulfolobus tokodaii.
                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                     1 VAEF 4
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NCBI_TaxID=4932;
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P32630;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               Signal
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UTR5_YEAST
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MEDLINE=2018606; PubMed=10731132;

MEDLINE=201860; R. Racher S.E., IN P. M. Hoskins R.A., Galle R.F.,

MEDLINE=201860; R. Racher S.E., IN P. M. Hoskins R.A., Galle R.F.,

MEDLINE R.G., Baxter E.G., Helt G., Champon M., Fedelifets B.D.,

MEDLINE R.M., Basud A., An H.-J., Andrews-Fannkoch C., Baldwin D.,

MEDLINE R.M., Basud A., Bandari D., Bolshakov S.,

Ballew R.M., Basud A., Bouck U., Broketein P., Blothakov S.,

Burris K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

Burris K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

Burris K.C., Busam D.A., Buller H., Davenport L.B., Davies P.,

Burris K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

Burris K.C., Busam D.A., Buller H., Cadieu E., Center R., Chandra I.,

Burris K.C., Busam D.A., Buller H., Cadieu E., Center R., Chandra I.,

Burris K.C., Busam D.A., Buller H., Cadieu E., Center R., Chandra I.,

Medson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J., Baragel A.B., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,

Adlali M., Ralvey D.A., Heiman T.J., Herrandez J.R., Houck J.,

Merkilov G., Milahin N.W., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murriby B., Murphy L., Murry D., Murriby D., Lais C.,

Shien B.C., Siden-Klamos I., Simpson M., Strong K., Smith T.,

Shies R., Tector C., Turner R., Venter E., Wang S.,

Millams S.M., Woodage T., Worlex E., Wang S., Shon H.,

Meng Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Welley R., P., Edver J., Schong W., Zhan M., Zhan G., Zhan C., Zhan C.,

Zhang J., Zhan K., Zhan G., Zhan M., Zhan G., Zhu X., Zhan L.,

Zheng X., Shier K., Zhong W., Zhan G., Zhu X., Zhu X., Zhan L.,

Zhang J., Zhan K., Zhan M., Zhan M., Z
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                                                                                                               Gaps
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MEDLINE=87086754; PubMed=3098981;
Shore E.M., Guild G.M.;
"Larval salivary gland secretion proteins in Drosophila structural analysis of the Sgs-5 gene.";
J. Mol. Biol. 190:149-158(1986).
                                                                                                                                                                                                                                                                                                           SGSS_DROME STANDARD; PRT; 163 AA.

SOSS_DROME STANDARD; PRT; 163 AA.

P07701; Q9VEIS;

10.1-APR-1988 (Rel. 07, Last sequence update)

10.0-CT-2003 (Rel. 42, Last annotation update)

Salivary glue protein Sgs-5 precursor.

SGSS OR CG7596.

Drosophila melanogaster (Fruit fly).

Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Chararyota; Drosophila, NCBI_TAXID=7227;
                                                                                                               ;
                                                                    Length 157;
                                                                                                            0; Indels
Riboflavin biosynthesis; Transferase; Complete proteome. SEQUENCE 157 AA; 17501 MW; 529558077E164A18 CRC64;
                                                                  Score 19; DB 1; L
Pred. No. 2.8e+02;
                                                                                                               0; Mismatches
                                                               Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                 14 VAEF 17
                                                                                                                                                       1 VAEF 4
                                                                                                                                                                                                                                                                      RESULT 32
3GS5_DROME
    38
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                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the "EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The gene clusters ARC and COR on chromosomes 5 and 10, respectively,
of Saccharomyces cerevisiae share a common ancestry.";
J. Mol. Biol. 233:372-388(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 19; DB 1; Length 163; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 18 POTENTIAL.
19 163 SALIVARY GLUE PROTEIN SGS-5.
163 AA, 18821 MW, 3A476FID3B06D864 CRC64;
                                Drosophila melanogaster.";
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
110-0CT-2003 (Rel. 22, Last amnotation update)
UTRS protein (Unknown transcript 5 protein)
UTRS OR YEL035C OR SYGP-ORF27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003718; AAF55436.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X04269; CAA27820.1; -.
                                                                   Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A24504; A24504.
FlyBase; FBgn0003375; Sgs5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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BFL1 MOUSE
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                                                                                                                                                                              MSRYGKNLVHYIIVEHDDQR -> MRDSNVKISVFPCALYN
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain 1.";
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
-!- FUNCTION: This protein is essential for replication of the chromosome. It is also involved in DNA recombination and repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Lidwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS9932. Q7UXV3;

15-MAR-2004 (Rel. 43, Created)

15-MAR-2004 (Rel. 43, Last sequence update)

15-MAR-2004 (Rel. 43, Last sequence update)

15-MAR-2004 (Rel. 43, Last annocation update)

Single-strand binding protein (SSB) (Helix-destabilizing protein).

SSB OR RB9917.

Rhodopirellula baltica.

Bacteria, Planctomycetes; Planctomycetacia; Planctomycetales;
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DNA-binding; DNA repair; DNA replication; Complete proteome
                                                                                                                                                                                                                                                                               100.0%; Score 19; DB 1; Length 166; 100.0%; Pred. No. 2.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                      RGNTTIN (IN REF. 1).
166 AA; 19335 MW; ASBEEBDOFAGD3DEA CRC64;
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  L22173; AAA34936.1; -. S65964; AAD13970.1; -. S66120; AAB28442.1; -. U18779; AAB65007.1; -.
                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
EMBL; L22173; AAA34936.
EMBL; S65964; AAD13970
EMBL; S66120; AAE28442
EMBL; U18779; AAE5507.
PIR; S50509; S50509.
Germonline; 139039; --
SGD; S0000761; UTES.
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     92 VAEF 95
                                                                                                                                                                                                                                                                                                                                                                                     1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                 MEDLINE-53346743; PubMed:8345191;
Lin E.Y., Orlofsky A., Berger M.S., Prystowsky M.B.;
"Characterization of Al, a novel hemopoletic-specific early-response
gene with sequence similarity to bcl-2.";
J. Immunol. 151:1979-1988(1993).
                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl-2-related protein Al (BFL-1 protein) (Hemopoietic-specific early
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                            MEDIJINE-98307518; PubMed-9645611;
Hatakeyama S., Hamasaki A., Negishi I., Loh D.Y., Sendo F.,
Nakayama K., Nakayama K.-I.;
"Multiple gene duplication and expression of mouse bcl-2-related
genes, Al.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 1; Length 172; 100.0%; Pred. No. 3e+02; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37AD35818E756488 CRC64;
172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALA/PRO-RICH.
BH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 116462; AAA16886.1; -.
EMBL; U23774; AAB97953.1; -.
EMBL; U23773; AAB97953.1; JOINED.
PIR; 149449; 149449.
HSSP; QO7817; INAZ.
MGD; MGI:102687; BG12ala.
InterPro; IPR000412; BG12_BH.
InterPro; IPR0004475; BGL2_Family.
PRT;
                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
""""INTN=CBA/J; TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PS50062; BCL2 FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
                                                                              response protein) (A1-A).
BCL2A1 OR BCL2A1A OR BFL1 OR A1.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19914 MW;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=129/Sv; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00452; Bcl-2;
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77
132 1
172 AA;
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Matches 4; Conserv
                                                                                                                                                NCBI_TaxID=10090;
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DOMAIN
SEQUENCE
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Gaps

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4; Conservative

28 VAEF 31

ESULT 35

1 VAEF 4

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WEDLINE-22388257; PubMed=12477932;

Ratausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

Alausner R.D., Collins F.S., Wagner L., Shemen C.R., Schuler G.D.,

Alatchenco L., Marusina K., Farmer R.A., Rubin G.M., Hong L.,

Alatchenco L., Marusina K., Farmer R.A., Rubin G.M., Hong L.,

Batchenco L., Marusina K., Farmer R.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibs R.A.,

Richards S., Worley K.C., Male S., Garcia A.M., Gibs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibs R.A.,

Richards S., Worley W., Sodergren B.J., Lu X., Gibs R.A.,

Richards W., Touchman J.W., Green B.D., Dickson W.C.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson W.C.,

Blakesley R.W., Touchman J.W., Gramucz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmucz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmucz J., Marra M.A.,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lang J.C.;
"GRS, a novel member of the Bcl-2 gene family, is highly expressed in multiple cancer cell lines and in normal leukocytes.";
Oncogene 14:997-1001(1997).
                                                                                                                          BFL1_HUMAN STANDARD; PRT; 175 AA.
Q16548; Q9524;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2014 (Rel. 43, Last annotation update)
Bcl-2-related protein Al (BFL-1 protein) (Hemopoietic-specific early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi S.S., Park I.-C., Yun J.W., Sung Y.C., Hong S.-I., Shin H.-S., "A novel Bcl-2 related gene, Bfl-1, is overexpressed in stomach cancer and preferentially expressed in bone marrow."; Oncogene 11:1693-1698(1995).
                                                                                                                                                                                                                                                                                    Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                              TISSUB=Umbilical vein;
MEDLINE=96184764; PubMed=8605321;
Karsan A., Yee E., Kaushansky K., Harlan J.M.;
Karonn of human Bel-2 homologue: inflammatory cytokines induce human Al in cultured endothelial cells.";
Blood 87:3089-3096(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97203281; PubMed=9050999;
Kenny J.J., Knobloch T.J., Augustus M., Carter K.C., Rosen C.A.,
Lang J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMITATICY).
-!- SUBCELLULAR LOCATION: Intracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96068895; PubMed=7478596;
                                                                                                                                                                                                                                      response protein) (GRS protein).
BCL2A1 OR BFL1 OR GRS OR BCL2L5.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=T-cell;
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                                    122 VAEF 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
-i- TISSUE SPECIFICITY: Seems to be restricted to the hematopoietic compartment. Expressed in peripheral blood, spleen, and bone marrow, at moderate levels in lung, small intestine and testis, a minimal levels in other tissues. Also found in vascular smooth muscle cells and hematopoietic malignancies.
-i- INDUCTION: By phorbol ester and inflammatory cytokines, such as TNF-alpha, or ILI-beta, but not by growth factors.
-i- SIMILARITY: Contains 1 BG1-2 homology 1 (BH1) domain.
-i- SIMILARITY: Belongs to the BG1-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-87222424; PubMed-3495534;
Dickey L.F., Sreedharan S., Theil B.C., Didebury J.R., Wang Y.-H.,
Kaufman R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1988 (Rel. 08, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
10-OCT-2003 (Rel. 42, Last annocation update)
Ferritin, middle subunit (Ferritin M) (Ferritin X) (Ferritin H').
Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N -> T (IN REF. 3).
Q -> H (IN REF. 3).
; 329D98AF2BE07A0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity, TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h Soore 19; DB 1; Le Similarity 100.0%; Pred. No. 3.1e+02; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALA/PRO-RICH.
BH1.
BH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 601056; -.
GO; 60008189; P:apoptosis inhibitor
GO; GO:0006916; P:anti-apoptosis; TAS.
InterPro; IPR000712; BGL2_BH.
InterPro; IPR002475; BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00452; BG1-2; 1.
SMART; SM00337; BCL; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 AL
97 BH
147 BH
72 N
107 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U29680, AACS0438.1; -.
EMBL, U27467; AACS0288.1; -.
EMBL, Y09397; CAA70566.1; -.
PMR, I39055, I39055.
HSSP, P53563; IAF3.
Geney, HGNC:991; BCLZA1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
77
132
12
107
175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 4; Conserv
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P07798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRI2_RANCA
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28-FEB-2003 (
28-FEB-2003 (
28-FEB-2003 (
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Matches
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                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outsition. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                 Ha Y., Shi D., Small G.W., Theil B.C., Allewell N.W., "Crystal structure of bullfrog M ferritin at 2.8 A resolution: "Crystal structure of bullfrog M ferritin at 2.8 A resolution: analysis of subunit interactions and the binuclear metal center."; J. Biol. Inorg. Chem. 4:243-256(1999).
-!- FUNCTION: Ferritin is an intracellular molecule that stores iron in a soluble, nontoxic, readily available form. The functional molecule, which is composed of 24 chains, is roughly spherical and contains a central cavity into which the polymeric ferric iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANBOUS: THERE ARE THREE TYPES OF PERRITIN SUBUNITS: L, M AND H CHAINS IN AMPHIBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 1; Length 176; 100.0%; Pred. No. 3.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the ferritin family. SIMILARITY: Contains 1 ferritin-like diiron domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1000; 22.-010.99.

InterPro; 1PR001519; Ferritin.
InterPro; 1PR001519; Ferritin.
InterPro; 1PR001519; Ferritin.
InterPro; 1PR0015040; Ferritin.
InterPro; 1PR001019; Ferritin.
InterPro; I
                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=99367924; PubMed=10439069;
the first processed in amphibia.";
J. Biol. Chem. 262:7901-7907(1987).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J02724; AAA49525.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        core is deposited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171
176 AA;
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Best Local Similarity
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STRAND
HELIX
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                                                                                                                                                                                                                                                                                                        Bao Q., Tian Y., Li W. Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the L10P family of ribosomal proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSBB PASMU STANDARD; PRT; 178 AA.
Q9LGB3; P57804;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Disulfide bond formation protein B (Disulfide oxidoreductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fuller T.E., Kennedy M.J., Lowery D.E.; aldentification of Pasteurella multocida virulence genes in septicemic mouse model using signature-tagged mutagenesis."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 177;
                                                                                                                      Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19591 MW; SODDCF896EF6F4E8 CRC64;
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100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0;
                          Last sequence update)
Last annotation update)
                                                                                                                                                   Thermoanaerobacteriaceae; Thermoanaerobacter NCBI _TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00362; -; 1.
InterPro; IPR011790; Ribosomal_L10.
InterPro; IPR012363; Ribosomal_L10eub.
Pfam; PF00466; Ribosomal_L10; IPPR01110; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; Complete protecome.
                                                                                                                                                                                                                                                                   STRAIN=MB4 / JCM 11007;
MEDLINE=21992816; PubMed=11997336;
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MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE013173; AAM25445.1; -.
                                                                            50S ribosomal protein L10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
(Rel. 41, G
(Rel. 41, I
(Rel. 41, I
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                                                                                                 RPLJ OR TTE2304
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Gaps

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Conservative

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1 VAEF 4 48 VAEF 177 AA.

STANDARD;

ESULT 38 L10_THETN D _RL10_THETN

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R EMBL; AF237925; AAF68411.1; -.

R EMBL; AE006038; AAR68411.1; -.

DR HAMAP; MF 00286; -; 1.

DR InterPro; IPR003752; DsbB.

DR Oxidoreductase; Redox-active center; Transport; Electron transport; KW Oxidoreductase; Redox-active center; Transport; Chapterone; Transmembrane; Interpretation transport; Chapterone; Transmembrane; Interpretation transport; Chapterone; Transmembrane; Interpretation transport; Carterior transport t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Klaembt C., Knust E., Tietze K., Campos-Ortega J.A.;
Closely related transcripts encoded by the neurogenic gene complex
enhancer of split of Drosophila melanogaster.";
EMBO J. 8:203-210(1989)
                                                                                                 Similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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DROWE

AC P13096; QSVBI8;

DT 01.JAN-1990 (Rel. 13, Last sequence update)

DT 01.JAN-1990 (Rel. 13, Last sequence update)

DT 15.MAR-2004 (Rel. 43, Last annotation update)

DT 15.MAR-2004 (Rel. 43, Last annotation update)

DR Enhancer of split m5 protein (E(spl)m5).

SN CG6096;

Drosophila melanogaster (Fruit fly).

C Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

C Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

C Ephydroidea; Drosophilidae; Drosophila.
FUNCTION: Required for disulfide bond formation in some periplasmic proteins. Acts by oxidizing the dsbA protein (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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REDOX-ACTIVE (BY SIMILARITY).
D2C45BB73B31F0BC CRC64;
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100.0%; Pred. No. 3.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                    (By similarity).
-!- SIMILARITY: Belongs to the dsbB family.
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MEDLINE=20196006; PubMed=10731132;
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1es 4; Conservative
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105
178 AA;
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Matches
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        THE STATE OF THE S
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Beandon R.C., Rogers Y.-H.C., Blazsi R.C., Champe M., Pfeiffer B.D., R.M. Bandon R.C., Romer C., Sancer B.J., Manuario D. Ballow B. M. Sand M. M. Bandario D. Bolabakov S. M. Ballow R. M. Bandario D. Bolabakov S. M. Bandario D. Borkova D. Borkova
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Retchum K.A., Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D., Retchum K.A., Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D., Reinardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J. Lee N.H., Sutton G.G. Gill S., Rirkness B.P., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McKell L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                  ö
TRANSFAC; T01644; -. FlyBase; FB970002631; ClucLeus; IDA. GO: GO: 0005634; ClucLeus; IDA. GO: GO: 0003677; F: DNA binding; IDA. InterPro; IPR001092; HLH basic. InterPro; IPR001092; HLH basic. InterPro; IPR00109; HLH; 1. SMART; SM00353; HLH; 1. SMART; SM00351; HLH; 1. SMART; SM00511; ORANGE; 1. DNA-binding; Differentiation; Neurogenesis; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                         100.0%; Score 19; DB 1; Length 178; 100.0%; Pred. No. 3.1e+02;
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Hypothetical protein; Signal; Complete proteome.
Hypothetical protein; Signal; Complete proteome.
SIGNAL
71 178 HYPOTHETICAL PROTEIN AFILLE.
                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                  ORANGE.
WRPW MOTIF.
19363D0F6043C84F CRC64;
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Archaeoglobaceae, Archaeoglobus.
                                                                                                                                                                                                                              BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein AF1118 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                Transcription regulation; Repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                         178 AA; 19923 MW;
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 VAEF 48
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B18_ARCFU
D_YB18_ARCFU
C_029147;
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                                                                                                                                                                                                                              DNA BIND
DOMAIN
                                                                                                                                                                                                                                                                                                           SEQUENCE
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CSTRAIN=35000HP / ATCC 700724;
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
A Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
In "The complete genome sequence of Haemophilus ducrey!.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
I "The complete genome sequence of Haemophilus ducrey!.";
C -- FUNCTION: Catalyzes a salvage reaction resulting in the formation of AMP, that is energically less costly than de novo synthesis.
C -- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-
D. Tiboses 1-diphosphate.
C -- CATALYTIC HOMOdimer (By similarity).
C -- SUBGUNIT: Homodimer (By similarity).
C -- SUBCLIDIAR LOCATION: Cytoplasmic.
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PROSTER; PSOOLO3; PUR PYR PR TRANSFER; 1.
Transferase; Glycosyltransferase; Purine salvage; Complete proteome.
Transferase; Glycosyltransferase; Purine salvage; Complete proteome.
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0
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
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                                                       100.0%; Score 19; DB 1; Length 178; 100.0%; Pred. No. 3.1e+02; ive 0; Mismatches 0; Indels.
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                                                                                                                                                                                                                                                                                                                                                                                                                               O7VRQ4,
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Adenine phosphoribosyltransferase (BC 2.4.2.7) (APRT).
APT OR HD1818.
19319 MW; 378A4F200240D924 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 19; DB 1; L
100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                        179 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; ME_00004; -; 1.
InterPro; IPR005764; Ade_phspho_trans.
InterPro; IPR002375; Pr/py_rp_transf.
InterPro; IPR000836; PRTransferase.
Pfam; PF00156; Pribosyltran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE017156; AAP96568.1; -.
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                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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   178 AA;
                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                  155 VAEF 158
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                                                                                                                                                                                       1 VAEF 4
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RETB BOVIN
ID RETB BOVIN
AC P18902;
                                                                                                                                                                                                                                                                                                                                                                                                        APT HAEDU
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MEDLINE=9366508; PubMedea496140;

MEDLINE=9366508; PubMedea496140;

A Zanotti G., Berni R., Monaco H.L.;

Trystal structure of liganded and unliganded forms of bovine plasma
"Crystal structure of liganded and unliganded forms of bovine plasma
"Trianch binding protein.";

L. Biol. Chem. 268:10728-10738(1933).

L. FUNCTION: Delivers retinol from the liver stores to the peripheral
tissues. In plasma, the RBP-retinol complex interacts with
transhbyretin, this prevents its loss by filtration through the
kidney glomeruli.

SUBCELLULAR LOCATION: Secreted.

L. SIMILARITY: Belongs to the lipocalin family.

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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              Zanotti G.; "I. sequence," The bovine plasma retinol-binding protein. Amino acid sequence, interaction with transthyretin, crystallization and preliminary X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Expression and cellular localization of retinol-binding protein messenger ribonucleic acid in bovine blastocysts and extraembryonic
                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY.

**RAY CRYSTALLOGRAPHY.

**Monaco H.L., Zanotti G.

**Three-dimensional structure and active site of three hydrophobic molecule binding proteins with significant amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                              MEDIJNE-93385352; PubMed-8373966;
Liu K.H., Dore J.J. Jr., Roberts M.P., Krishnan R., Hopkins F.M.,
Godkin J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00061; lipocalin; 1.-
PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
Plaama; Vitamin A; Retinol-binding; Transport; Liver; Lipocalin;
                                                                                                                                                                                                                          MEDLINE=91006139; PubMed=2209607;
Berni R., Stoppini M., Zapponi M.C., Meloni M.L., Monaco H.L.,
Zanotti G.;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
02-FCB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein (PRBP) (RBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUB; IFEM; 01-NOV-94.
PDB; IFEN; 01-NOV-94.
INTERPRO; IPR002345; Lipocalin.
InterPro; IPR000566; Lipocin_cytFABP.
                                                                                                                                                                                                                                                                                                                                        Eur. J. Biochem. 192:507-513(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3iol. Reprod. 49:393-400(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iopolymers 32:457-465(1992).
                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE OF 52-183 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, S65585, AAB28336.1;
PIR, 146955, 146955.
PIR, S13186, S13186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1ERB; 31-JAN-94.
1HBP; 31-JAN-94.
1HBQ; 31-JAN-94.
1FEL; 01-NOV-94.
                                                                                              taurus (Bovine).
                                                                                                                                                                NCBI TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MEDLINE=95202115; PubMed=7894745;
BOULTINE=95202115; PubMed=7894745;
BOULTAIS K., Nirgianaki A., Onyango P., Savakis C.;
BOULTAIS K., Nirgianaki A., Onyango P., Savakis C.;
BOULTAIS K., Nirgianaki A., Onyango P., Savakis C.;
Infection and expolamanic incompatibility among laboratory strains.";
Insect Mol. Biol. 3:131-142(11994).
Insect Mol. Biol. Biods to the origin of replication it binds specifically double-stranded DNA at a 9 bp consensus (dnaA box): 5-TTATC(C/A/A/C/A)A-3. DnaA binds to ATP and to acidic phospholipids (By similarity).
Insect Mol. SIMILARITY: Belongs to the dnaA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wolbachia sp.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales, Rickettsiaceae, Wolbachieae, Wolbachieae, Wolbachia.
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 19; DB 1; Length 183; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
03-JUN-1994 (Rel. 29, Last amonotation update)
Chromosomal replication initiator protein dnaA (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                     21068 MW; D6BA064CB9E67C09 CRC64;
               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                  183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VAEF 4
3D-structure.
DISULFID
DISULFID 7
DISULFID 12
HELIX
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P35907;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDILINE 88007612; PubMed=2820981; MEDILINE=88007612; PubMed=2820981; Kurowski B., Ludwig B.; Kurowski B., Ludwig B.; "The genes of the Paracoccus denitrificans bc1 complex. Nucleotide sequence and homologies between bacterial and mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ubiquinol-cytochrome C reductase iron-sulfur subunit (EC 1.10.2.2)
(Rieske iron-sulfur protein) (RISP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gubunits.";
J. Biol. Chem. 262:13805-13811(1987).
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
-!- FUNCTION: Complex III or cytochrome b-c1 complex), which is a complex (complex denial that generates an electrochemical potential respiratory chain that generates an electrochemical potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytochrome c1 and the Rieske protein.
-!- SUBCELLULAR LOCATION: Membrane-bound.
-!- MISCELLANEOUS: The Rieske protein is a high potential 2Fe-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ferrocytochrome c.
-!- COFACTOR: Binds 1 2Fe-2S iron sulfur cluster per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paracoccus denitrificans.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.
NCBI_TaxID=266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coupled to ATP synthesis. CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 19; DB 1; Length 186; 100.0%; Pred. No. 3.3e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                 186 AA; 21283 MW; C423C06CEFFB0459 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.
-!- SIMILARITY: Belongs to the Rieske family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 AA.
                                                                                                                                                       PRINTS; PRO0051; DNAA; PARTIAL.
PROSITE; PS01008; DNAA; PARTIAL.
DNA replication; DNA-binding; ATP-binding.
NON TER 18 18
SQÜENCE 186 AA; 21283 MW; C423C06CEFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005805; Rieske.
InterPro; IPR005806; Rieske dom.
InterPro; IPR006317; Rieske_proteo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
EMBL; Z28981; CAA82285.1; -.
PIR; S39317; S39317.
HAMAP; MF_00377; -: 1.
INTERPC; IPR001957; Bac_DnaA.
Pfam; PF00308; bac_dnaA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M17522; AAA25571.1; -. EMBL; X05799; CAA29243.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A29413; A29413.
HSSP; P13272; 1RIE.
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 VARF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VAEF 4
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CRI PARDE
D UCRI PARDE
C P05417;
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-!- FUNCTION: CAN EFFICIENTLY HYDROLYZE NONSTANDARD NUCLEOTIDES SUCH
AS XTP TO XMP OR ITP TO IMP, BUT NOT THE STANDARD NUCLEOTIDES. XTP
IS THE BEST SUBSTRATE.
-!- CATALYTIC ACTIVITY: NTP + H(2)O = NDP + phosphate.
-!- COFACTOR: Magnesium or manganese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=JAL-I DSN 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087;
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Googyne J.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Googyne J.D., Kerlavage A.R., Doughberty B.A., Tomb J.-F., Adams M.D., Reich C.I., Goothagen N.S.M., Weidman J.F., Fuhrmann J.L., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.M., Banna M.C., Cotton M.D., Roberts M.A., Kaine B.P., Borodovsky M., Cotton M.D., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hwang K.Y., Chung J.H., Kim S.-H., Han Y.S., Cho Y.; structure-based identification of a novel NTPase from Methanococcus
                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                 TIGREAMS; TIGRO1416; Rieske_proteo; 1.
TIGREAMS; TIGRO1409; TAT signal_seq; 1.
PROSITE; PSO0200; RIESKE_1; 1.
PROSITE; PSO0200; RIESKE_2; 1.
Blectron transport; Inner membrane; Transmembrane; Metal-binding; Iron; 2Fe-2S; Oxidoreductase.
TRANSMEM 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Nucleoside-triphosphatase (EC 3.6.1.15) (Nucleoside triphosphate
phosphohydrolase) (NTPase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 100.0%; Score 19; DB 1; Length 190; Local Similarity 100.0%; Pred. No. 3.38+02; hes 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           F83F5D9A9C1FBEE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                IRON-SULFUR (2FB-2S) (IRON-SULFUR (2FB-2S) (

    -!- SUBUNIT: Homodimer.
    -!- SIMILARITY: Belongs to the HAM1 NTPase family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-99332061; PubMed=10404228;
                                                                                                                                                                                                                                                                                                                                134 IRC
152 IRC
155 IRC
154 BY
20299 MW; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanococcus jannaschii
InterPro; IPR006311; Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                       134
152
155
137
137
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Q57679;
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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NTPA METJA
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"Complete genome sequence of the alkaliphilic bacterium Bacillus
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                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; B27758; RPECRS.
HSSP; P03012; 2RSL.
                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                              14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                             1 VAEF 4
                                                                                                                                                                                                                                                                                                     TNRO ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                 TNRO_ECOLI
                                                                                                                                                                                                                                                                                      RESULT 48
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                    SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 19; DB 1; Length 193; 100.0%; Pred, No. 3.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus halodurans.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                             22202 MW; 3570565E007D3DAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HAM1 protein homolog 2.
                                                     EMBL; U67478; AAB98211.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                           PIR, C64328; C64328.
PDB; 1B78; 28-JAN-00.
PDB; 2MJP; 28-JAN-00.
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                             193 AA;
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halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
-1- SIMILARITY: Belongs to the HAM1 NTPase family.
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=562,
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SEQUENCE 194 AA, 21868 MW, BBC5A0C4F19A04B3 CRC64;
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01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transposon Th2501 resolvase.
                                                                                                                                                                                                                                                                                                                                                            EMBL; AP001517; BAB06786.1; -.
PIR; C84033.
RASP; O57679; 1B78.
HAWAR; MF_01405; -; 1.
InterPro; IPR002637; Hamlp_like.
Pfan; PP01725; Hamlp_like; 1.
ProDom; PD004952; Hamlp_like; 1.
PIGRFAMS; TIGRO0042; TIGRO0042; 1.
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Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,

Asia H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,

Kasai H., Kashimoto K., Kitakawa M., Kitagawa M.,

Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,

Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,

Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,

"A 570-kb DNA sequence of the Escherichia coli K-12 genome

corresponding to the 28.0 40.1 min region on the linkage map.";

DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 41, Last annotation update)
Purative DNA invertase from lambdoid prophage Qin.
PINQ OR B1545.
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INQ ECOLI
D PINQ ECOLI
C P77170;
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        InterPro; InterPro; HTH 7.
InterPro; IPR006119; Recombinase.
InterPro; IPR006119; Recombinase.
InterPro; IPR006119; resolvase_N.
Pfam; PF00739; HTH 7; 1.
PROSITE; PS00399; RECOMBINASES_1; FALSE_NEG.
PROSITE; PS00399; RECOMBINASES_2; 1.
Hypotherical protein; DNA recombination; DNA integration; DNA-binding; DNA invertese; Complete proteome.
ACT_SITE 11 IL TRANSIENT COVALENT LINKAGE TO DNA DURING
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STRAND CLEAVAGE AND REJOINING
(BY STMILARITY).
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SEQUENCE FROM N.A.
MEDLINE-97426617; PubMed-9278503;
MIDLINE-97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Maynew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden J.R., Rose D.J.,
Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 19; DB 1; Length 196; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 41, Last amnotation update)
18-EEB-2003 (Rel. 40, Last amnotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 196 AA; 21852 MW;
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us-09-594-978a-2.rsp

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MEDLINE=93315143; PubMed=7686882;
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                                                                                                                                                                                                         Pfam; PF02796; HTH 7; 1.
Pfam; PF00239; resolvase; 1.
PROSITE; PS00397; RECOMBINASES_1; FALSE_NEG.
PROSITE; PS00398; RECOMBINASES_2; 1.
Hypothetical protein; DNA recombination; DNA-binding;
                                                                                                                                                                                                                                                                   TRANSIENT COVALENT LINKAGE TO DNA DURING
STRAND CLEAVAGE AND REJOINING
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
17-anscriptional regulatory protein uhpA.
UHPA OR B3669 OR C4593 OR Z5159 OR ECS4606 OR SF3792 OR S3976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                           100.0%; Score 19; DB 1; Length 196; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                         643A62BC940B29A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 AA
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SPECIES=E.coli; STRAIN=K12 / MG1655;
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NCBI TaxID=562, 217992, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Friedrich M.J., Kadner R.J.;
"Nucleotide sequence of the uhp r.
J. Bacteriol, 169:3556-3563(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES=E.coli;
MEDLINE=87279903; PubMed=3301805;
                                                                                                                                          PIR; A64888; A64888.
HSSP; P03012; ZRSL.
EcoGene; E013372; pinR.
InterPro; IPR006120; HTH 7.
InterPro; IPR006118; Recombinase.
InterPro; IPR006119; resolvase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 174:2754-2762(1992)
                                                                                                                                                                                                                                                                invertase; Complete proteome.
                                                                                                          EMBL; AE000234; AAC74456.1; -.
EMBL; D90775; BAA14979.1; -.
EMBL; AE016764; AAN81596.1; -.
                                                                                                                                                                                                                                                                                                          196 AA; 21908 MW;
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Escherichia coli 06,
Escherichia coli 0157:H7, and
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ses 4; Conservative
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   family
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P10940;
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SPECIESES.COLI, STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohrsubo E., Nakayama K., Marata T., Tanaka M., Tobe T., Kuhara T., Tanaka M., Tobe T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Asumaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Secherichia coli moomple sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
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                                                                                                                                                                                                                            SECURNCE FROM N.A.
SPECIES=E.coli, STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=1247157;
MEICH R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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-!- PTM: PHOSPHORYLATED BY UHPB (PROBABLE).
-!- SIMILARITY: Contains 1 response regulatory domain.
-!- SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
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Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.; "DNA sequence and analysis of 136 kilobases of the Escherichia cogenome: organizational symmetry around the origin of replication-genomics 16:551-564 (1993).
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SEQUENCE FROM N.A.
SPECIES=E.Coll; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Fosfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECIES. S. ELEXNET; STRAIN=2457T / ATCC 700930 / Serotype 2a; SPECIES. S. Elexner; STRAIN=2457T / ATCC 700930 / Serotype 2a; MEDLINE=2259074; PubMed=12704152; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; Runyen-Janecky L.J., Zhou S., Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."; Infect. Immun 71:2775-2786(2003).

Infect. Immun 71:2775-2786(2003).

TRANSCRIPTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
Transcriptional regulatory protein uhpA.
Transcriptional regulatory protein uhpA.
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Island M.D., Wei B.-Y., Kadner R.J.;
"Structure and function of the uhp genes for the sugar phosphate
transport system in Escherichia coli and Salmonella typhimurium.'
J. Bacteriol. 174:2754-2762(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100.0%; Score 19; DB 1; Length 196; Similarity 100.0%; Pred. No. 3.4e+02; 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                     EMBL; L10328; AAA62021.1; -...
EMBL; AE01044; AAC6692.1; -...
EMBL; AE0106596; AAC58868.1; -...
EMBL; AE0105596; AAC58868.1; -...
EMBL; AE0105596; AAC58868.1; -...
EMBL; AE01599; AAC1896.1; -...
EMBL; AE015991; AAP18964.1; -...
PIR; A26225; BVECAU.
PIR; P1204; P91204; P
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EcoGene; EG11051; unpl.
InterPro; IPR000792; HTH LuxR.
InterPro; IPR001789; Response_reg.
Pfam; PF00196; GerE; I.
Pfam; PF00072; response_reg; 1.
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MEDLINE=92234930; PubMed=1569007;
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NCBI_TaxID=602;
                                                                                                                                                                                                            EMBL; M17102; AAA24720.1; -.
EMBL; M89479; AAA24724.1; -.
EMBL; L10328; AAA62021.1; -.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 VAEF 33
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HPA_SALTY
O_UHPA_SALTY
C_P27667;
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Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: APPEARS TO BE THE POSITIVE ACTIVATOR OF UHPT TRANSCRIPTION.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- PTM: PHOSPHORYLATED BY UHPB (PROBABLE).
-!- PTM: PHOSPHORYLATED BY UHPB (PROBABLE).
-!- SIMILARITY: Contains 1 response regulatory domain.
-!- SIMILARITY: BELONGS TO THE LUXR/UHPR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-99303612; PubMed=10373455;
Muramatsu M., Sankaranand V.S., Anant S., Sugai M., Kinoshita K.,
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2B-FEB-2003 (Rel. 41, Last sequence update)
2B-FEB-2003 (Rel. 41, Last annotation update)
Activation-induced cytidine deaminase (EC 3.5.4.5) (Cytidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 19; DB 1; Length 196; 100.0%; Pred. No. 3.48+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                     EMBL; M89480; AAA27243.1; -.
EMBL; AE008876; AAL22648.1; -
PIR; A41853; A41853.
HSSP; P10957; IRNL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                    Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 4; Conserv
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AICD MOUSE
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1 VAEF 4
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ACT_SITE
SEQUENCE
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RETB_HORSE
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                                                                                                                 for efficient antibody responses.
-- CATALYITC ACTIVITY: CYtidine + H(2)0 = uridine + NH(3).
-- COPACTOR: Zinc (By similarity)
--- SIMILARITY: Belongs to the cytidine and deoxycytidylate deaminases
                                                        J. Biol. Chem. 274:18470-18476(1999).
--- FUNCTION: RNA-editing deaminase involved in somatic hypermutation, gene conversion, and Class-switch recombination. Required for several crucial steps of B-cell terminal differentiation necessary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=20165948; PubMed=10701121;
MEDLINE=20165948; PubMed=1.0701121;
Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,
Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D.,
Davidson N.O., Honjo T.; "Specific expression of activation-induced cytidine deaminase (AID), a "Specific expression of activation-induced cytidine deaminase family in germinal center B novel member of the RNA-editing deaminase family in germinal center B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
16-DEC-1998 (Rel. 41, Last annotation update)
Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP synthase glutanine amidotransferase subunit) (IGP synthase subunit hisH) (IMCP synthase subunit hisH) (IMCP synthase subunit hisH) (IMCP synthase subunit hisH) (IMCP SSO0600 OR CO8_GOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGUENCE FROM N.A.
STRAIN-ATCC 38092 / DSM 1617 / P2;
MEDLINE-9735708; PubMed=9209067;
Charlebois R.L., Sensen C.W., Doolittle W.F., Brown J.R.;
"Evolutionary analysis of the hisGGABGFDEHI gene cluster from the archaeon Sulfolobus solfataricus P2.";
J. Bacteriol 179:4429-4432 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 1; Length 198; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                   EMBL, AF132979; AAD41793.1; -.

MGD; MGI:1342279; Aicda.

GO; GO:004125; F:cytldine deaminase activity; IDA.

InterPro; IPR07094; APOBEC C.

InterPro; IPR002125; GCMP/Cyt_deam.

Pfam., PR05240; APOBEC C.; 1.

PROSITE; P800903; CYT_DCMP_DEAMINASES; 1.

MENA processing; Hydrolase; Zinc.

METAL

87

ZINC (BY SIMILARITY).

METAL

90

90

ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 AA; 24030 MW;
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 VAEF 97
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                                                                                                                                                                              family.
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HISS SULSO
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 55022 / DSM 1617 / P2;

MANAYER ATCC 35022 / DSM 1617 / P2;

MANAYER ATCC 35022 / DSM 1617 / DSC 2502 / DSC
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Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q., St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F., Ragan M.A., Sensen C.W.,
                                                                                                                                                                               "Gene content and organization of a 281-kbp contig from the genome the extremely thermophilic archaeon, Sulfolobus solfataricus P2."; Genome 43:116-136 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00117; GATase; 1.
PROSITE; PS00442; GATASE TYPE I; FALSE NEG.
Histidine biosynthesis; Transferase; Glutamine amidotransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17DB1A86724CE095 CRC64;
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100.0%; Pred. No. 3.5e+02;
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BY SIMILARITY.
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178 BN
180 BN
22533 MW;
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HAMAP; MF 00278; -; 1.
InterPro; IPR000991; GATase_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE006689; AAK40911.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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199 AA;
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ACT_SITE 76
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                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
             Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, U21208; AAC48461.1;
PIR; 146257; 146257
HSSP; P27485; 1AQB.
InterPro; IPR00245; Lipocalin.
InterPro; IPR00266; Lipocalin.
Prair; P700061; Lipocalin.
PRINTS; P800179; LIPOCALIN.
PROSITE; P800213; LIPOCALIN.
PROSITE; P800213; LIPOCALIN; 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Signal; Lipocalin.
SIGNAL.
SIGNAL.
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PLASNA RETINOL-BINDING PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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19 201 PL
22 178 BY
86 192 BY
138 147 BY
201 AA; 23022 MW;
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Best Local Similarity 100...
4, Conservative
Equus caballus (Horse)
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ETB HUMAN
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MEDLINE=2238857; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.D., Feingold E.A., Grouse L.H., Schaefer C.F., Ehat N.K.,

Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raha S.S., Loquellano N.E., Petres G.J., Abramson R.D., Mullahy S.J.,

B Rownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

B Rosak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunarane P.H.,

B Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Du X., Gibbs R.A.,

B Rahay J., Helton E., Ketteman M., Madan A., Kodrigues S., Sanchez A.,

Mutting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Hakesley R.W., Touchman J.W., Grantz B.D., Dickson M.C.,

B Nutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Chnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Mann A., Schein J.E., Jones S.J.M., Marra M.A.,

Munn and mouse CDNA sequences "I. S. M. Marra M.A.,

Munn A., M.A., Schein J.E., Solies C. Moore than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            He F.; "Functional prediction of the coding sequences of 79 new genes deduced "Functional prediction of the coding sequences of 79 new genes deduced by analysis of cDNA clones from human fetal liver."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE.
MEDLINE-95395382; PubMed=7666002;
Jaconi S., Rose K., Hughes G.J., Saurat J.-H., Siegenthaler G.;
Jaconi S., Rose K., Hughes G.J., Saurat J.-H., Siegenthaler G.;
McDaracterization of two post-translationally processed forms of human serum retinol-binding protein: altered ratios in chronic renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Fetal liver;
Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural and functional studies of vitamin A-binding proteins."; Ann. N.Y. Acad. Sci. 359:79-90(1981).
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MEDLINE=86055755; PubMed=2998779;
D'Onofrio C., Colantuoni V., Cortese R.;
Structure and cell-specific expression of a cloned human retinol binding protein gene: the 5'-flanking region contains hepatoma specific transcriptional signals.";
EMBO J. 4:1981-1989(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 19-201, AND DISULPIDE BONDS.
MEDLINE-88019004; PubMed-2444024;
Rask L., Anundi H., Fohlman J., Peterson P.A.;
"The complete amino acid sequence of human serum retinol-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 19-201.
MEDLINE-81254137; PubMed-6942701;
Rask L., Anundi H., Boehme J., Eriksson U., Ronne H., Sege K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=80004132; PubMed=573217;
Rask L., Anundi H., Peterson P.A.;
"The primary structure of the human retinol-binding protein.";
PEBS Lett. 104:55-58(1979).
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MEDLINE-91017499; PubMed=2217163;
retinol-binding protein.";
Nucleic Acids Res. 11:7769-7776(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jps. J. Med. Sci. 92:115-146(1987)
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                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein."
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"Crystallographic refinement of human serum retinol binding protein at 2-A resolution.";

Cowan S.W., Newcomer M.E., Jones T.A.;

Proteins 8:44-61(1990).

TTR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANCE-17-199.
DISEASE: Defects in RBD4 are a cause of retinol-binding protein DISEASE: Defects in RBD4 are a cause of retinol-binding protein deficiency [MIM:180250]. This condition causes night vision problems. It produces a typical "fundus xerophthalmicus," featuring a progressed atrophy of the retinal pigment epithelium. DISEASE: A deficiency of vitamin A blocks secretion of the binding protein posttranslationally and results in defective delivery and supply of vitamin to the epidermal cells (a condition associated with a dermatosis).
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MEDLINE=99103495; PubMed=9888420;
Seeliger M.W., Biesalski H.K., Wissinger B., Gollnick H., Gielen S.,
Frank J., Beck S., Zrenner E.,
Frank J., Gielen S.,
Frank J., Giel
                                                                                                                                                                                                                                                                                                                                                                                                                          "The structure of human retinol-binding protein (RBP) with its carrier protein transthyretin reveals an interaction with the carboxy terminus of RBP.";
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                                                                                                                                                            MEDLINE=92322903; PubMed=1623143;
Monaco H.L., Zanotti G.;
"Three-dimensional structure and active site of three hydrophobic
molecule-binding proteins with significant amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  With a Carliagory to the lipocalin family. SIMILARITES. NAME-Mutations of the RBP4 gene; NOTE-Retina International's Scientific Newsletter;
                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH MEDLINE=99162254; PubMed=10052934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Invest. Ophthalmol. Vis. Sci. 40:3-11(1999).
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EMBL; X02775; CAA26553.1; -
EMBL; X02775; CAA26553.1; -
EMBL; X02824; CA846699.1; -
EMBL; AF119868; AAF69622.1; ALT_INIT.
EMBL; AF025334; AAC02945.1; -
PIR; A93494; VAHU.
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                                                                                                                                                                                                                                                                                   similarity.";
Biopolymers 32:457-465(1992)
                                                                                                                                      K-RAY CRYSTALLOGRAPHY
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T-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS), AND REVISIONS TO 134 AND 185. MEDLINE-98437649, PubMed=9757135, Zanotti G., Panzalorto M., Marcato A., Malpeli G., Folli C., Berni R.; "Structure of pig plasma retinol-binding protein at 1.65-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABOURNCE FROM N.A.
MEDLINE-92131064; BAUMGG=1723146;
Trout W.E., McDonnell J.J., Kramer K.K., Baumbach G.A., Roberts R.M.;
Trout W.E., McDonnell J.J., Kramer E.K., Baumbach G.A., Roberts R.M.;
"The retinol-binding protein of the expanding pig blastocyst:
molecular cloning and expression in trophectoderm and embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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                                                                   00; G0:0005615; C:extracellular space; TAS.
G0; G0:0005501; F:retinoid binding; TAS.
InterPro; IPR002345; Lipocalin.
InterPro; IPR000566; Lipocalin.
Pfam; PR00061; Lipocalin.
Pro; PR00061; Lipocalin.
PRINTS; PR00013; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN.
Lipocalin; Diseas mutation; Vision; 3D-structure.
SIGNAL
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/FIId=VAR_009276.
G -> D (in RBP deficiency).
/FIId=VAR_009277.
F -> L (IN REF. 1 AND 3).
LGSGR -> WAA (IN REF. 1 AND 3).
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15-UUL-1998 (Rel. 36, Last sequence update)
16-Rel. 36, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP)
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PDB; 1BRP; 31-JAN-94.
PDB; 1BRQ; 31-JAN-94.
PDB; 1QAB; 09-APR-99.
SWISS-2DPAGE; P02753; HUMAN.
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Best Local Similarity 100.
Matches 4; Conservative
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                                        Siena-2DPAGE; P02753; -
Genew; HGNC:9922; RBP4.
MIM; 180250; -.
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MEDILINE-88207643; PubMed=3838985;

A MEDILINE-88207643; PubMed=3838985;

A MEDILINE-88207643; PubMed=3838985;

A MEDILINE-88207643; PubMed=3838985;

A Bjoerck L., Erikson U., Aakerstroem B., Jones A., Newcomer M.,

B Joerck L., Rask L.;

Tetinol-binding proceins.

I J. Biol. Chem. 260:6422-6480 (1985).

- I- FUNCTION: Delivers retinol from the liver stores to the peripheral tissues. In plasma, the RBP-retinol complex interacts with transthyretin, this prevents its loss by filtration through the kidney glomeruli.

C - SUBCELLULAR LOCATION: Secreted.

- SUBCELLULAR LOCATION: Secreted.

- SUBCELLULAR LOCATION: Correted.
                                                        Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=93011736; Pubmed=1339354;
MEDLINE=91011736; Pubmed=1339354;
"The lacrimal gland synthesizes retinol-binding protein.";
Exp. Rye Res. 55:163-171(1992).
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP).
                                                                                                                                                                                                                         SEQUENCE OF 19-201.
                                                                                                       NCBI_TaxID=9986;
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 PIR; A39486; A39486.

PDB; 1A0B; 28-JAV-98.

InterPro; IRR002145; Lipocalin.

InterPro; IRR002145; Lipocalin.

Fan; PR00061; Lipocalin; 1.

FRINTS; PR00179; LIPOCALIN.

PROSITE; PS00213; LIPOCALIN; 1.

PLASMA; VItamin A; Retinol-binding; Transport; Liver; Signal; Lipocalin; 3D-structure.
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PLASMA RETINOL-BINDING PROTEIN.
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100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0;
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201 AA;
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PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; l.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Lipocalin;
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                                                                                                                                                                                                                                                                                                                                                                   PLASMA RETINOL-BINDING PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19; DB 1; Length 201;
Pred. No. 3.50+02;
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yigz.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                          EMBL; S45958; AAB23582.1; -.
PIR; A49178; VARB.
HSSP; P18902; 1FEN.
InterPro; IPR002345; Lipocalin.
InterPro; IPR00566; Lipocln_cytFABP.
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YIGZ OR B3848.
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P27862;
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Gaps ő

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201 AA.

PRT;

RETB RABIT STANDARD; P06912; 01-JAN-1988 (Rel. 06, Created)

ETB RABIT
D RETB R.
C P06912
T 01-JAN ESULT 58

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                                                                                                                                                                                                                                            MEDIJNE=54147996; PubMed=8313894;
Koonin E.V., Bork P., Sander C.;
"Yeast chromosome III: new gene functions.";
EMBO J. 13:493-503(1994).
-!- SIMILARITY: BELONGS TO THE UPF0029 FAMILY. STRONG, TO H.INFLUENZAE
HI0722.
                                                    SEQUENCE FROM N.A.
STRAIN=RIZ / MG1655;
MRDLINE=2338024; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Eschichha coli genome: DNA sequence of the region Efrom 84.5 to 86.5 minutes";
Science 257:771-778(1992).
                                                                                                                                                                 MEDLINE=91057145; PubMed=2243799;
Nakahigashi K., Inokuchi H.;
Nucleotide sequence between the fadB gene and the rrnA operon from
Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
         Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitchic spindle assembly checkpoint protein MAD2A (MAD2-like 1) (HSMAD2).
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ENGLA ST. Y192.

ECOGene; EG11484; Y192.

InterPro; IPR001902; EFG III V.

InterPro; IPR001498; UPF0029; 1.

Pfam; PF01205; UPF0029; 1.

TIGREAMS; TIGR0027; TIGR00257; 1.

PROSITE; PR00110; UPF0029; 1.

HYPOTHETICAL protein; Complete proteome.

L -> V (IN REF. 2).

125 125 L -> V (IN REP. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 205 AA.
                                                                                                                                                                                                               Nucleic Acids Res. 18:6439-6439(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M87049; AAA67645.1; ALT INIT.
EMBL; AE000460; AAC76851.1; ALT INIT.
EMBL; X54687; CAA38501.1; ALT_INIT.
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                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 VAEF 185
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                                 NCBI_TaxID=562;
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Q13257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klebert S., Barnikol-Watanabe S., Kratzin H.D., Hilschmann N.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
[1]
SEQUENCE FROM N.A.
MEDLINE=96421709;
MEDLINE=96421709;
Li Y., Benezra R.,
"Identification of a human mitotic checkpoint gene: hsMAD2.";
Science 274:246-248(1996).
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Luo X., Fang G., Coldiron M., Lin Y., Yu H., Kirschner M.W.,
Wagner G.;
                                                                                                                                                                                                                                                                                                                                                                                                Jin D.-Y., Jeang K.-T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nobori T.;
Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23598 MW;
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4; Conservative
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205 AA;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                    NCBI_TaxID=10090;
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MAD2L1 OR MAD2A
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                         -i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE MAD2 FAMILY.
-i- SIMILARITY: Contains 1 HORMA domain.
-i- DATABASE: NAME-Atlas Genet. Cycgenet. Oncol. Haematol.;
WWW-"http://www.infobiogen.fr/services/chromcancer/Genes/MAD2L1ID304.html".
                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its word non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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092185; Q9JT63;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Mitotic spindle assembly checkpoint protein MAD2A (MAD2-like 1).
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SUBUNIT: INTERACTS WITH CDC20 AND WITH ADAM17 (TACE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO, GO:0005699; C:kinetochore; TAS.
GO, GO:0005699; C:kinetochore; TAS.
GO; GO:0007067; P:mitocic checkpoint; TAS.
CO: GO:00700793; P:mitocic checkpoint; TAS.
InterPro: IPRO03511; DNAbind_HORMA.
PROSITE; PS50815; HORMA; 1.
Cell cycle; Mitosis; Nuclear protein; 3D-structure.
F DOMAIN 14 197
F STRAND 11 12
STRAND 15 15
HELIX 17 17 17
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EMBL; AD000186; CAA03943.1; --
EMBL; BC00516; AAH00356.1; --
EMBL; BC005945; AAH05945.1; --
PIR; G01942; G01942.
PDB; LDUJ; 08-MAR-00.
Genew; HGNC:6763; MADZLI.
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185 1
205 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               checkpoint protein Mad2.";

(call 101:635-645(2000).

-!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND DELAYS THE ONEST OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. I INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20348739; PubMed=10892650;
Dobles M., Liberal V., Scott M.L., Benezra R., Sorger P.K.;
"Chromosome missegregation and apoptosis in mice lacking the mitotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
Jin D.-Y., Jeang K.-T.;
"Identification of a novel component of the spindle assembly checkpoint in mammalian cells.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 1; Length 205; 100.0%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U83902; AADD9238.1; -.

REMBL; AF261919; AAF69525.1; -.

REMBL; AF261919; AAF69525.1; -.

REMBC; G013257; 1DUJ.

REMBC; G013257; 1DUJ.

REMBC; G013257; 1DUJ.

REMBC; G010000776; C: Kinetcochore; IDA.

REMBC; G010000776; C: Rinitotic chromosome segregation; IMP.

REMBC; G010000077; C: Rinitotic spindle checkpoint; IMP.

REMBC; G010000078; P: Rinitotic spindle checkpoint; IMP.

REMBC; G010000078; PORMA; 1.

REMBC; G010000078; REMBC; RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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C -> S (IN REF. 1).
T -> I (IN REF. 1).
A9F3F28BC4C9738E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAPHASE PLATE (BY SIMILARITY).
--- SUBGNIT: INTERACTS WITH CDC20.
--- SUBCELLULAR LOCATION: Nuclear (By similarity).
--- SIMILARITY: BELONGS TO THE MADZ FAMILY.
--- SIMILARITY: CONtains 1 HORMA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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YACI LEGEN
ID YACI LEGEN
AC P37033;
DT 01-UTN-1994
DT 16-OCT-2001 (
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D71119;
15-DEC-1998 (Rel. 37, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Uname oxygenase (EC 1.14.99.3).
                                                                                      Bacteriol. 175:5666-5676(1993).
                                             STRAIN=Philadelphia 1;
MEDLINE=93374864; PubMed=8366052;
Mengaud J.M., Horwitz M.A.;
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97158681; PubMed=9006041; Schmitt M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 179:838-845(1997).
                                                                                                                                                          EMBL; L22081; AAA25294.1; -.
                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                PIR, A48642, A48642.
Hypothetical protein
SEQUENCE 208 AA;
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   45 VAEF 48
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1717;
                                                                                                                                                                                                                       1 VAEF 4
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                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE=96005047; PubMed=7561763; McGarvey P.B., Tousignant M., Geletka L., Cellini F., Kaper J.M.; McGarvey P.B., Tousignant M., Geletka L., Cellini F., Kaper J.M.; "The complete sequence of a cucumber mosaic virus from Ixora that is deficient in the replication of satellite RNAs."; J. Gen. Virol. 76:2257-2270 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
E -> K (IN REF. 1).
A -> V (IN REF. 1).
A -> GS (IN REF. 1).
N -> H (IN REF. 1).
-!- FUNCTION: Allows the bacteria to use the host heme as an iron source. Involved in the oxidation of heme and subsequent release of iron from the heme moiety.
-!- CATALYTIC ACTIVITY: Heme + 3 AH(2) + 0(2) = biliverdin + Fe(2+) + CO + 3 A + 3 H(2)0.
-!- SIMILARITY: Belongs to the heme oxygenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; BRNA positive-strand viruses, no DNA stage; Bromoviridae;
Cucumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60D9E8E2ED7ED456 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last amnotation update)
Coat protein (Capsid protein) (CP).
Cucumber mosaic virus (strain Ixora) (CMV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000247; Cucumovirus_coat.
InterPro; IPR008975; Viral_cap_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U73860; AAC44832.1; -. EMBL, U73860; AAC44832.1; -. HASP, P09601; 1028. InterPro; IPR002051; Heme_oxygenase. Pfam; FF01126; Heme_oxygenase; 1. PRINTS; PR00088; HAEWCXCHAASE. PROSITE; PR00593; HEME_OXYGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 IN
34 E
60 B
93 DC
192 N
24116 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U20219; AAC54619.1; -.
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60
92
192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 VAEF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COAT CMVIX
Q66120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family
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CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                              "The major iron-containing protein of Legionella pneumophila is an aconitase homologous with the human iron-responsive element-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Declarate Entry N.A., Stratistics of Stratistics of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                             Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
NCBI_TaxID=446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium diphtheriae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 1; Length 208; 100.0%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .l protein.
208 Aa; 23714 MW; 1E5C75E63A20C800 CRC64;
      Hypothetical 23.7 kDa protein in acn 5'region.
Legionella pneumophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Gaps

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The sequence of the Orgyia pseudoteugata multinucleocapsid nuclear polyhedrosis virus genome."; 
Virology 229:1381-399(1997).
-!- FUNCTION: COULD BE INACTIVE AS THE ACTIVE SITE CYSTEINE IS MODIFIED TO TRYPTOPHAN.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. CDC14 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                                                                            Gaps
                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                              Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 1; Length 220; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels
                                                                                          100.0%; Score 19; DB 1; Length 218; 100.0%; Pred. No. 3.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUIVALENT OF ACTIVE SITE CYS. D3FC093F1953D425 CRC64;
                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Putative protein-tyrosine phosphatase 1 (EC 3.1.3.48).
                                                              218 AA; 24185 MW; 130E82D17BD75224 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U75930; AAC59009.1; -.
Interpro; IPRO00387; TYR phosphatase.
PROSITE; PS00383; TYR PHOSPHATASE 1; FALSE_NEG.
PROSITE; PS50036; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                      220 AA.
Pfam; PF00760; Cucumo_coat; 1.
PRINTS; PR00222; CUCUMOCOAT.
ProDom, PD001284; Cucumovirus_coat; 1.
Coat protein.
SEQUENCE 218 AA; 24185 MW; 130E82D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SÎTE 162 162 E
SEQUENCE 220 AA; 25234 MW;
                                                                           Query Match
Best Local Similarity Tou.v.
Best A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                        96 VAEF 99
                                                                                                                                                            1 VAEF 4
                                                                                                                                                                                                                                                                      NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase.
                                                                                                                                                                                                                                                                    PTP1 NP1
010274;
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETRAIR=984915, White O., Nelson K.E.,
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Klenk H.-P., Clayton R.A., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Kerlavage A.R., Des N.H., Sutton G.G., Gill S.,
Kliknes E.F., Dougherty B.A., Moreamey K., Adams N.D., Loftus B.,
Kliknes E.F., Dougherty B.A., Moreamey K., Adams N.D., Loftus B.,
Peterson S., Reich C.I., Moweil L.K., Badger J.H., Glodek A., Zhou L.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBDAIT: Component of the archaeal exosome multienzyme ribonuclease complex (Potential).
-!- SUBGELULAR LOCATION: (Stoplasmic (Potential).
-!- SIMILARITY: Contains 1 KH domain.
-!- SIMILARITY: Contains 1 S1 motif domain.
                                                                                                                       Archaeoglobus fulgidus.
Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 AA; 24725 MW; A11B7F1A26972833 CRC64;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable exosome complex RNA-binding protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50084; KH_TYPE_1; 1.
PROSITE; PS50126; S1; 1.
Exceome; RNA-binding; Complete proteome.
DOMAIN 135 127 S1 MOTIF.
DOMAIN 135 193 KH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF 06623; -; 1.
InterPro; IPR004089; KH dom.
InterPro; IPR004089; KH type_1.
InterPro; IPR008994; Nucleic_acid_OB.
InterPro; IPR003029; S1.
Pfam; PF00573; S1; 1.
SMART; SM00322; KH; 1.
SMART; SM00322; KH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001070; AAB90745.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; D69311; D69311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 VAEF 212
                                                                                                                                                                                                       NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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RESULT 67 RAN_TETPY

PRT; 223 AA.

STANDARD;

ESULT 66 CR1 ARCFU D ECR1 ARCFU .C 029758;

AUE

139 VAEF 142

1 VAEF 4

10-OCT-2003 (Rel. 42, Created)

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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 VAEF 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VAEF 4
                              NCBI_TaxID=274;
                                                                                                                                                                                                                                                 H(+)(Out)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAN TETTH P41915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nozawa Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 69
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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VATD THETH

1D VATD THETH

AC 087880,

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2004 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE V-type ATP synthase subunit D (EC 3.6.3.14) (V-type ATPase subunit D).

GN ATPD OR VATD.

OS Thermus thermophilus.
                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GTP-binding nuclear protein RAN/TC4.
Tetrahymena pyriformis.
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
NCBI_TaxID=5908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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Nagata K.-I., Takemasa T., Alam S., Hattori T., Watanabe Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 1; Length 223; 100.0%; Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
IBB (BY SIMILARITY).
W, 5474DADB5ABF0977 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO0231; small GFP; 1.
PROSITE; PS01115; RAN; 1.
GTP-binding; Nuclear protein; Protein transport
 223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, D21825, BAA04849.1; -.
HSSP, P17080; 1A2K.
InterPro; IPR002041, RAN.
InterPro; IPR001806; RAB trnsfrmig.
InterPro; IPR005225; Small_GTP.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 126 GT
128 143 IB
223 AA; 25422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO05225; Small_GTP-
Pfam; PF00071; ras; 1.
PRINTS; PR00627; GTPRANTC4.
PRINTS; PR00449; RASTENSFRWNG.
SWART; SM00176; RAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 4, Conserv
                                                                                                                                                                                SEQUENCE FROM N.A.
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RAN TETPY P41914;
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NP BIND
NP BIND
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SET THE TRANSPORT OF TH

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 144:123-125(1994).
-!- FUNCTION: GTP-binding protein involved in nucleocytoplasmic transport. Required for the import of protein into the nucleus and also for RNA export. Involved in chromatin condensation and control of cell cycle (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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-1- SUBCELLULAR LOCATION: Nuclear (By similarity)
-1- SIMILARITY: Belongs to the small GTPase superfamily. Ran family.
                                                                                                                                                                                                           "V-type H+-ArPase/synthase from a thermophilic eubacterium, Thermus thermophilus. Subunit structure and operon."; J. Biol. Chem. 275:13955-13961(2000).
                                                                                                                                                                                                                                                                                                                   gradient across the membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding low-M(r) (GBLM) protein, Ran/TC4, from micronucleated Tetrahymena thermophila and amicronucleated Tetrahymena pyriformis.";
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                            Yokoyama K., Ohkuma S., Taguchi H., Yasunaga T., Wakabayashi T.,
Yoshida M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Nagata K.-I., Takemasa T., Alam S., Hattori T., Watanabe Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 223;
                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the V-ATPase D subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Match
Local Similarity 100.0%; Pred. No. 3.98+02;
Les 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01813; ATP-synt_D; 1.

ProDom; PD004122; ATPsynt Deub; 1.

TIGRRAMS; TIGR00309; V. ATPase subD; 1.

Hydrclase; ATP synthesis; Hydrogen ion transport.

SEQUENCE: 223 AA; 24677 MW; B666AE00DFE0B08B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-F8B-2003 (Rel. 41, Last annotation update)
GTP-binding nuclear protein RAN/TC4.
Tetrahymena thermophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 AA
                                                                                                                  STRAIN=HB8 / ATCC 27634;
MEDLINE=20250964; PubMed=10786522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D63799; BAA33198.2; -.
HAMAP; MF_00271; -; 1.
InterPro; IPR002699; ATPSYnt_Dsub.
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MEDILINE-89293088; PubMed=2661722;
GONDART A.F., Blisgard G.W., Rohrmann G.F.;
GCARACTERIZATION of the genetic organization of the HindIII M region of the multicapsid nuclear polyhedrosis virus of Orgyia pseudotsugata reveals major differences among baculoviruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1997 (Rel. 35, Last annotation update)
101-MOV-1997 (Rel. 35, Last annotation update)
Hypothetical 26.0 kDa protein in PP34-EXO intergenic region (ORF 4).
Orgyia pseudostagate multicapsid polyhedrosis virus (OpWNPV).
Viruses, dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; Virology 229:381-399(1997).
-!- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 1; Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69F8B8409AF703F8 CRC64;
                                                                                                                                                                                                                                                                                                   HISTORY I PROCESSES AND INTERPRETATION INTERPRETATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gen. Virol. 70:1815-1828(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 126 G
128 143 II
225 AA; 25649 MW;
                                                                                                                                                                                                                                                          EMBL; D17748; BAA04600.1; -. HSSP; P17080; 1A2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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P24080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Pyridine nucleotide biosynthesis; Transferase; Nucleotidyltransferase; NAD; Complete protecome.
NAD; Complete protecome. 4CF04E8F70E48941 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NAAD) (By similarity).
-!- CATALYTIC ACTIVITY: ATP + nicotinate ribonuclectide = diphosphate
+ deamido-NAD(+).
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

BEDILNE-22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nartins dos Sancos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Martins dos Sancos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazacz A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lubber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                         10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-20103 (Rel. 42, Last annotation update)
10-0CT-20104 (Rel. 42, Last annotation update)
10-0CT-20104 (RC 2.7.7.18)
10-0MIAD(-NAD(-) pyrophosphorylase) (Deamido-NAD(+) diphosphorylase)
(Nicotinate mononucleotide adenylyltransferase) (NaMN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Mirobiol. 4:799-808(2002).
-!-FUNCTION: Catalyzes the reversible adenylation of nicotinate monomucleotide (NaMN) to nicotinic acid adenine dinucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                   ll protein; Late protein.
228 AA; 25962 MW; F0766AD21F60039D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: NAD biosynthesis.
-!- SIMILARITY: Belongs to the nadD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_00244; -; 1.
InterPro; IPR004820; Cytidylyltransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas putida (strain KT2440).
             EMBL, D13796; BAA02952.1; -.
EMBL, D13929; BAA03030.1; -.
EMBL, U75930; AAC59129.1; -.
PIR, D30857; D30857.
Hypothetical protein; Late pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE016792; AAN70379.1; -.
                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adenylyltransferase).
                                                                                                                                                                             Best Local Similarity
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Q88DL5;
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                            RESULT 71
NADD_PSEPK
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STANDARD;

COREF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast.
Bukaryota, Rhodophyta, Bangiophyceae, Bangiales; Bangiaceae, Forphyra.
NCBL_TaxID=2787;
                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reith M.E., Munholland J.; "Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flant Moi. Biol. Rep. 13:333-335 (1995).
-!- SUBDUAT: Part of the 30S ribosomal subunit.
-! SUBCELLULAR LOCATION: Chloroplast.
-!- SUBLIARITY: Belongs to the 33P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
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   100.0%; Score 19; DB 1; Length 230; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 30S ribosomal protein S3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U38804; AAC08194.1; -.
Query Match
Best Local Similarity 100.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porphyra purpurea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                42 VAEF 45
                                                                                                                            1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                   RR3_PORPU
P51308;
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RR3 PORPU
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                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 13:1572-1579(2003).
--- FUNCTION: Methyltransferase required for the conversion of dimethylmenaquinone (DKHZ2) to menaquinone (WHHZ) (By similarity).
--- CATALYTIC_ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                  Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Sojobosi T., "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Menaquinone biosynthemism methyltransferase ubiE (EC 2.1.1.-).
                                                                                                                                  Bacteria; Actimobacteria; Actinobacteridae, Actinomycetales;
Corynebacterines Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amortation update)
Menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UBIE OR CGL0471.

Corynebacterium glutamicum (Brevibacterium flavum).

Corynebacterian Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 1; Length 230; 100.0%; Pred. No. 4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MP_01813; -; 1.
InterPro; IPR001601; Methyltransf.
InterPro; IPR001601; SAM bind.
InterPro; IPR0004033; UDiE/COO5_Metrf.
Pfam; PF01209; UDie methyltran; 1.
PROSITE; PS01183; UBIE J. PALSE NEG.
PROSITE; PS01184; UBIE 2; PALSE NEG.
Menaquinone biosynthesTs; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 AA; 25366 MW; E10DCB602A1CD886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s-adenosyl-L-homocysteine + menaquinol.
-!- PATHWAY: Menaquinone biosynthesis; last step.
-!- SIMILARITY: Belongs to the ubiE family.
                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
MEDLINE=2272375375; PubMed=12840036;
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es 4; Conservative 0
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SEQUENCE 230 AA;
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                                                                                                                UBIE OR CE0481.
                                                                                                                                                                                                                                                                                                                                                                                      efficiens.";
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QBNT39;
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UBIE_CORGL
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Matches
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RESULT 73 UBIE_COREF

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                            "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Methyltransferase required for the conversion of
dimethylmenaquinone (DMH12) to menaquinone (MKH2) (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES-E. coli, STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503,
Blattner F.R., Plunkert G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECTES=E.coli;
MEDLINE=92223101; PubMed=1314093;
Yang T.-P., Depew R.E.;
"Nucleotide sequence of a region duplicated in Escherichia coli toc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                 EMBL; AP005275; BAB97864.1; -.
HAMAP. MF 01813; -; 1.
Interpro; IPR001601; Methyltransf.
Interpro; IPR000515; SAM bind.
Interpro; IPR0004033; UbiE/COQ5_Metrf.
Pfam; PF01209; Ubie methyltran; 1.
PROSITE; PS01183; UBIE 2; FALSE NEG.
PROSITE; PS01184; UBIE 2; FALSE NEG.
Menaquinone biosynthesis; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 230 AA; 25244 MW; A8548173B7901400 CRC64;
                                                                                                                s-adenosyl-L-homocysteine + menaquinol.
-!- PATHWAY: Menaquinone biosynthesis; last step.
-!- SIMILARITY: Belongs to the ubiz family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P24195;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein yals.
YGIB OR B3037 OR C3783 OR SF3077 OR S3282.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutants.";
Biochim. Biophys. Acta 1130:227-228(1992).
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NCBI_TaxID=562, 217992, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli,
Escherichia coli 06, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 VAEF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VAEF 4
                  Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGIB ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                         SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928; MEDLINE=2238824; PubMed=12471157; MeDLINE=2238824; PubMed=12471157; MeDLINE=2238824; PubMed=12471157; MedLine, R. Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin Q., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a; MEDLINE=22590274; PubMed=12704152; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786(2003).
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EMBL, AE016766, AAN95227.1; -.
EMBL, AE016986, AAN95257.1; -.
EMBL, AE016986, AAN9368.1; -.
PIR, S22360; S22360.
EGOGGER, EG1164; yglB.
Hypothetical protein; Complete proteome.
SEQUENCE 234 AA; 24868 MW; 08D5DE931072C966 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Q88891 agrobacteri
Q898x7 bradyrhizob
Q8009 pyrococcus
Q86535 hepatitis a
Q8476 listeria mo
Q9476 listeria mo
Q9476 listeria mo
Q9476 listeria mo
Q9476 listeria mo
Q9520 sulfolobus
Q8000 sulfolobus
Q9127 bacillus an
Q9127 bacillus an
Q9127 bacillus an
Q9127 bacillus an
Q91368 streptomyce
Q8565 mycobacteri
Q9538 streptomyce
Q8561 mycobacteri
Q9531 mycobacteri
Q9531 mycobacteri
Q9531 mycobacteri
Q9511 neurospora
Q81x6 corynebacteri
Q9011 neurospora
Q81x6 corynebacteri
Q9133 mycobacteri
Q1343 molluscum c
Q8663 pseudomonas
Q86512 caenothabdi
Q9813 byrococcus
Q86513 byrococcus
Q82xi2 nitrosomona Q8xx11 ortxa sativ Q8xx11 ortxa sativ Q8xpx corynabacte Q8nup0 salmo salar P97252 escherichia Q97144 clostridium Q82xx0 streptomyce Q82xx0 streptomyce Q82xx0 tartebonyce Q852x darobacteri Q89816 bradythizob Q8yul6 bradythizob Q8xx16 collamydphi Q7vpv6 chlamydphi Q7vpv6 chlamydphi Q7vyy9 bacteriopha Q9550 nitrosomona Q91185 arabidopsis Q97x3 homo sapien Q96Eb2 ambloplites 
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O8v203 pyrococcus
O8cd94 mus musculu
O9dw67 rat cytomeg
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Q7xlw4 oryza sativ
Q9exg6 listeria mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q865E2
Q98SR3
Q98SR3
Q91315
P95437
O69133
Q8TYL3
Q8TYL3
Q9Y5V1
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Q9CDX1
Q8IX12
Q98IX12
Q98IX12
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Q8d064 yersinia pe Q8aqg5 bacteroides Q7wm22 bordetella Q7wm29 bordetella Q8tdn7 homo sapien Q94049 pinus taeda Q8tdc1 homo sapien Q15953 drosophila Q8s16 oryza sativ Q91zx8 rattus norv	005364 actinobacil Q83y72 gamma-prote Q8ayq2 zea mays (m Q8bw25 mus musculu Q9a8y3 caulobacteri Q8u757 agrobacteri Q80x21 pseudomonas Q8zxk1 pyrobaculum Q8t4t4 aedes aegyp Q8n0v8 aedes aegyp	Q81413 aedes aegyp Q84145 aedes aegyp Q16900 aedes aegyp Q16900 aedes aegyp Q840149 oryza sativ Q840149 oryza sativ Q8101498 mus musculu Q71136 atdus norv Q81510 corymebacte Q70415 bordetella Q70415 bordetella Q70415 bordetella Q70415 corymebacte Q70413 corymebacte Q70413 corymebacte	090214 Canis famil 021312 tetrahymena 021312 tetrahymena 07unx6 rhodopirell 08gyrs lactobacill 08gyrs lactobacill 08gyrb babesia equ 017131 babesia equ 09typo babesia equ 09typo babesia equ 09typo babesia equ 09typo babesia equ	Q9tya8 babesia equ Q4636 babesia equ Q9ty3 babesia equ Q45145 caenorhabdi Q9f511 Erreptomyce Q2043 caenorhabdi Q8t4XI mus musculu Q8t4XI mus musculu Q8t4XI mus musculu Q8tXU2 pyrobaculum Q8tXU3 methanopyru Q20303 caenorhabdi Q8d64S mus musculu Q8d64S mus musculu Q9A121 streptococc Q94b20 streptococc Q94b20 streptococc Q8f513 corynebacte Q8f513 corynebacte Q8f513 leptospira Q87wstl bordeella	U98112 fnlzobum 1 Q99728 clostridium Q82wil nitrosomona Q18536 caenorhabdi
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Q9R5C0;
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Matches
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                      Q81ag7 arabidopsis
99727 arabidopsis
99727 aratus norv
99727 aratus norv
997216 arachaecolob
03168 arachaecolob
03567 2ymomonas m
030400 neisseria a
Q7423 mortierella
Q81c35 mortierella
Q81c35 mortierella
Q81c0 escherichia
Q81c1 mus musculu
Q82c1 mus musculu
Q84c0 escherichia
Q81g1 shigella
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Q81g1 methanosarc
Q8c07 methanosarc
Q8c1 methanosarc
Q8c1 methanosarc
Q8f1s9 corynebacte
Q81s9 corynebacte
Q81s3 corynebacte
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Q81s3 arabidopsis
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X MEDLINE-94039144; PubMed=7693466;

Lutz F., Mohr M., Grimmig M., Leidolf R., Linder D.;

Lutz F., Mohr M., Grimmig M., Leidolf R., Linder D.;

T erythrocyce membranes cytotoxin-binding protein in rabbit

T erythrocyce membranes. An oligomer of 28 kDa with similarity to

T transmembrane channel proteins ";

Eur. J. Biochem. 217:1123-1128(1993).

R PIR, S39049; S39049.

R HSSP; P47865; J44N.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016310; P:transporter activity; IEA.

R GO; GO:0006310; P:transporter activity; IEA.

R InterPro. IPRO00225; MIP.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytocxin-binding protein (Fragment).
Oryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Q854X2
Q81AA7
Q81Z34Z
Q81Z34Z
Q81Z34Z
Q81Z34Z
Q81Z35
Q81Z3
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Q7WX56
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Pfam; PF00230; MIP;
SEQUENCE 20 AA; 2
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ID Q9TS18
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Bukoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
NCBI_TaxID=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                            in
                                                                                                                                                                                                                                                                                          "Multiple copies of genes coding for electron transport proteins
the bacterium Nitrosomonas europsea.";
J. Bacteriol. 175:2445-2447(1993).
SEQUENCE 22 AA; 2549 MW; C22664FSERICE75F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Protein database for several tissues derived from five instar of
                                                                                           Bacteria, Proceedacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadacee, Nitrosomonadacee, Nitrosomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                             MEDLINE-93224468; PubMed-8385668;
McTavish H., LaQuier F., Arciero D., Logan M., Mundfrom G.,
Fuchs J.A., Hooper A.B.;
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 22;
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Local Similarity 100.0%; Score 19; DB 2; Length 22
Local Similarity 100.0%; Pred. No. 3.46+02;
Nes 4; Conservative 0; Mismatches 0; Indels
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MEDLINE-21177481; PubMed=11280994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin regulatory light chain 2 (MLG-2) (Fragment).
Bombyx mori (Silk moth).
Ol-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 14, Last annotation update)
Cytochrome P-460 (Fragment).
Nitrosomonas europaea.
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Pred. No. 4.7e+02;
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Best Local Similarity
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EMBL; AE009770; AAL62822.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 35 AA; 3934 MW; A324B4F94F6A14BB CRC64;
                                                                         Match 100.0%; Score 19; DB 17; Local Similarity 100.0%; Pred. No. 5.4e+02; tes 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008199; F:ferric iron binding; IEA.
GO; GO:0006879; P:iron ion homecetasis; IEA.
GO; GO:0006826; P:iron ion transport; IEA.
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Equus caballus (Horse)
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SEQUENCE FROM N.A.
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STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Rleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Loftus B., Richardson D., Zhou L., Kirkness B.F., Peterson S., Loftus B., Rizagerald L.M., Lee N., Adams M.D., Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin B., Venter J.C.,
    Gaps
                                                                                                                                                                                                                                                                                                             Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRALTHAZ / ATCC 51768 / DSM 7523;
MEDLINE-21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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    Indels
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Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
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EMBL; AE000596; AAD07920.1; -.

PIR; G64625; G64625.

TIGR; HP0847.

Hypothetical protein; Complete proteome.

SEQUENCE 33 AA; 3704 MW; FA3F52631C0DB943 CRC64;
                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein HP0847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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    0; Mismatches
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PAE0485.
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    4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                             13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 VABF 18
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                                      1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=210;
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Matches
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Gaps
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Giffard J.M., Brandon R.B., Bell T.K.,
"Further identification of single nucleotide polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klebsiella pneumoniae.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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Length 35;
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                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equine transferrin gene.";
submitted (SEP-199) to the EMBL/GenBank/DDBJ databases.
EMBL; AF185722; AAF05508.1;
EMBL; AF185722; AAF05501.1;
EMBL; AF185724; AAF05503.1;
EMBL; AF185725; AAF05503.1;
EMBL; AF185725; AAF05503.1;
EMBL; AF185725; AAF05504.1;
EMBL; AF185725; AAF05506.1;
EMBL; AF185726; AAF05506.1;
EMBL; AF185728; AAF05506.1;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Q7UXLS
ID Q7UXLS
                                                                                                  025478
                           RESULT 9
025478
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                                                                                                                                                                                         The dharpart Sepsis,

RTAINFANTC 25955;

RA SKrally F.A., Willard B.L., Cameron D.C.;

RT "The dha regulon of Klebsiella pneumoniae.";

STRAINFANTC 25955;

RI "The dha regulon of Klebsiella pneumoniae.";

SUBMILLEG (UTL-1955) to the EMBL/GenBank/DDBJ databases.

LE SUBMILLEG (UTL-1955) to the EMBL/GenBank/DDBJ databases.

PUBL: SUBMILLEG LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -:- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).

DR REML: W10303; AAA74224.1; -- THE MIP/AQUAPORIN FAMILY (TC 1.A.8).

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR HYDOCH PROMOQ25; MIP-family; 1.

RHYDOCH PROMOG25; MIP-family; 1.

RHYDOCH PROMOGE P
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STRAIN=VBS3 / ATCC 700802;
MEDLINE=22550857; PubMed=1265927;
MEDLINE=22550857; PubMed=1265927;
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tetterlin H., Dodson R.J., Umayam L., Brinkec L., Beanan M.,
Daugherty S., DeBOY R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Ulterback T., Radune D., Retchum K.A., Dougherty B.A., Fraser C.M.;
Entercoccus faecalis.";
                                   Willard B.L.;
"Investigation of the Klebsiella pneumoniae 1,3-propanediol pathway:
"Investigation and expression of glycerol dehydratase and 1,3-
propanediol oxidoreductase.";
Thesis (1994), Chemical Engineering, University of Wisconsin-Madison.
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó,
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SEQUENCE 45 AA, 5278 MW, 89CB55FSCB4C014A CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q830H9;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 19; DB 2; I
100.0%; Pred. No. 6.8e+02;
iive 0; Mismatches 0;
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IIGR; EF2805; -.
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Best Local Similarity 100...
4; Conservative
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EF2805.
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Best Local Similarity
STRAIN=ATCC 25955;
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MEDILINE 97394467; PubMed=9222185;
MEDILINE 97394467; PubMed=9222185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Gill S., Dougherty B.A.,
Teleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Lofttus B., Richardeon D., Dodgson R., Khalak H.G., Glodek A.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Pujii C., Bowman C., Watthey L., Wallin E.,
Venter J.C.,
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                                                                                                                                                                                                                                       Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the gastric pathogen Helicobacter
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Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
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100.0%; Score 19; DB 16; Length 48;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pylori.";
Mature 388:39-547(1997).
Mature 388:39-547(1997).
Mature 388:39-547(1997).
Mature 388:39-547(1997).
PIR, E64618; E64618.
PIR, E64618; E64618.
Hypothetical protein; Complete proteome.
SEQUENCE 48 AA; 5492 MW; ED5911D96F57BFEB CRC64;
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EMBL: BX294135; CAD71991.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 51 AA; 5951 WW; 60F62389COFDA6A7 CRC64;
                                                     01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-07N-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein HP0789.
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Last annotation update)
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PRELIMINARY;
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Best Local Similarity 100.
Matches 4; Conservative
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32 VAEF 35
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Q8FIF3
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Nature 409:529-533 (2001).
BERL, ABG05369; AAG56425.1; -.
PINE, E85745; E85745.
Hypothetical protein; Complete protecome.
SEQUENCE 54 AA; 6507 MW, 8BEFACD8BE6140CE CRC64;
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Bacteria, Firmicutes; Bacillales; Paenibacillaceae, Brevibacillus.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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STRAIN=0157:H7 / EDD933 / ATCC 700927;
STRAIN=0157:H7 / EDD933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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           Pred. No. 7.8e+02;
; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 100.
Matches 4; Conservative
           Best Local Similarity 100.
Matches 4, Conservative
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                                                                                                                                                                                       31 VAEF 34
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01-NOV-1996
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FRAIN-OG.HI / CFT073 / ATCC 700928;

MEDLINE-2238824; Pubmed=1247157;

MEDLINE-238824; Pubmed=1247157;

MEINE A., BURLAID V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Bercherichia coll.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
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EMBL, AF386526; AAL72547.11, -.

GO, GO:0046821; C:extrachenosomal DNA; IEA.

Hypothetical protein; Plasmid.

SEQUENCE 61 AA; 6858 MM; FICCI7B10B28CBFC CRC64;
                                                                                                                                                                                                                                            Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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SEQUENCE 54 AA; 5322 MW; 6B3C3D0F21ED4376 CRC64;
                                                     Last sequence update)
Last annotation update)
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100.0%; Pred. No. 8.2e+02;
tive 0; Mismatches 0;
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PRT;
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01-MAR-2002 (TrEMBLrel. 20, C:
01-MAR-2002 (TrEMBLrel. 20, Li
01-OCT-2003 (TrEMBLrel. 25, Li
Hypothetical protein.
CP0186.
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Query Match
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Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McChtchen B.F.,
Presnail J.K., Herrmann R., Dolan M., Tingey S., Hu Z.-H., Vlak J.M.;
"Genome sequence analysis of Helicoverpa zea single nucleocapsid
                                              Gaps
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Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                          Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SPECIES-Helioccoverpa armigera nucleopolyhedrovirus G4;
Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.;
"Sequence analysis of the gpJ7 gene of Heliothis armigera single-nucleocapsid nucleoplyhedrovirus.";
Zhongguo Bingduxue 15:35-42(2000).
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0
100.0%; Score 19; DB 2; Length 61; 100.0%; Pred. No. 9.3e+02; ive 0; Mismatches 0; Indels
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01-JUN-2001 (TERMELTE1. 17, Last sequence update)
01-JUN-2001 (TERMELTE1. 17, Last sequence update)
01-OCT-2003 (TERMELTE1. 25, Last annotation update)
ORF49 (Hypothetical protein) (Unkown).
Helicoverpa armigera nucleocopyhedrovirus G4, and
Helicoverpa armigera nucleopolyhedrosis virus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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SPECIES-Heliocoverpa armigera nucleopolyhedrovirus G4,
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Last annotation update)
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                                                                                                                                                                                                                                           61 AA.
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01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
PRO2435.
                                              4; Conservative
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Query Match
Best Local Similarity
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                                                                                                                                54 VAEF 57
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SPECIES-Heliocoverpa armigera nucleopolyhedrovirus G4;
MEDLINB=21078302; PubMed=11210934;
Wang H., Chen X., Wang H., Arif B.M., Vlak J.M., Hu Z.;
"Nucleotide sequence and transcriptional analysis of a putative basic DNA-binding protein of Helioverpa armigera polyhedrovirus.";
Virus Genes 22:113-120(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-Helicoverpa armigera nuclear polyhedrosis virus;
Fang M., Hu Z., Chen X., Vlak J.M.;
"Genetic organization of the HindIII-L region of Helicoverpa armigera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Zhang C.X., Jin W.R.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=Cl;
Pubmed=12050807;
Wang H., Hu Z., Sun X., Vlak J.M., Chen X.; "Sequence analysis of the iap3 gene of Heliothis armigera single-nucleocapsid nucleocolynedrovirus."; Zhongguo Bingduxue 15:43-49(2000).
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MEDLINE=21064569; PubMed=11125177;
Chen X., IJKel W.: Tarchini R., Sun X., Sandbrink H., Wang H
Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;
"The sequence of the Hellocoverpa armigera single-nucleocapsid
nucleopolyhedrovirus genome.",
J. Gen. Virol. 82:241-257(2001).
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Chen X, IJKel W.F., Tarchini R., Sun X., Sandbrink H., Wang
Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;
Submitted (MAY-Z000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single-nucleocapsid nucleopolyhedrovirus.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR334030; AAL561941;
EMBL; AR201059; AAG5627911;
EMBL; AR26694; AAK66298.1;
Hypochetical protein.
SEQUENCE 68 AA; 7962 MW; 61B7718BFBB195FF CRC64;
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01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Helix-turn-helix protein, CopG family.
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nes 4; Conserv
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NO SER PRESENCE OF SERVICE OF SER

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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, APPOSESO, ABB93300.1;
Hypothetical protein; Complete proteome.
SEQUENCE 69 AA; 7815 MW; COEZA072C2295DDZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Str.1, Str.2, Str.3, Str.4, Str.9, Str.10, and Str.11;
MEDLINE=22135992; PubMed=12140239;
Antunes A., Templeton A.R., Guyomard R., Alexandrino P.;
"The role of nuclear genes in intraspecific evolutionary inference: genealogy of the transferrin gene in the brown trout.";
Mol. Biol. Evol. 19:1272-1287(2002).
EMBL; AF488859; AANI7027.1; -.
EMBL; AF488849; AANI7027.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferrin (Fragment).

Salmo trutta (Brown trout).

Bukaryota; Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
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Last annotation update)
                          Corynebacterium glutamicum (Brevibacterium flavum).
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0;
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EMBL, AF488857, AAAL 1032.11, --

EMBL, AF488857, AANL 1032.11, --

EMBL, AF488855, AANL 1032.11, JOINED.

EMBL, AF488855, AANL 1037.11, JOINED.

EMBL, AF488873, AANL 1042.11, JOINED.

EMBL, AF4888914, AANL 1042.11, JOINED.

EMBL, AF488911, AANL 1068.11, JOINED.

EMBL, AF488921, AANL 1073.11, JOINED.

EMBL, AF488921, AANL 1073.11, JOINED.

EMBL, AF488921, AANL 1073.11, JOINED.

EMBL, AF488921, AANL 1078.11, JOINED.

EMBL, AF488929, EMBL, AF488921, AANL 1078.11, JOINED.

EMBL, AF488929, EMBL, AF488921, GANL 1078.11, JOINED.

GO, GO: 0005576; C: extracellular; IEA.

GO, GO: 0006879; F: fear: icn no homeostasis; IEA.

GO, GO: 0006826; P: icn ion homeostasis; IEA.

GO, GO: 0006826; P: icn ion transport; IEA.
                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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PRINTS; PR0422; TRANSFERRIN.
NON_TER 71 71
SEQUENCE 71 AA; 7546 MW; 81
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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OBAUO2;
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EMBL;
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BMBL, AL731599; CARGESS21.; -

SENBL, AL731599; CARGESS21.; -
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                                                                                                              SEQUENCE FROM N.A.
STRAINS-TCC 19718 / IFO 14298;
MEDLINE-22586410; PubMed=12700255;
MEDLINE-22586410; PubMed=12700255;
Ghain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
"Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautocroph Nitrosomonas europaea.";
EMBL: MX21897; CAD84200.1; -.
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01-0CT-2003 (TrENBLrel. 25, Last sequence update)
01-0CT-2003 (TrENBLrel. 25, Last sequence update)
0S-0CT-2003 (TrENBLrel. 25, Last annotation update)
0SJNBA0044M19.22 protein (OSJNBA0053B21.1 protein).
0SJNBA0044M19.22 OR OSNBA0053B21.1.
0STARATOTA SALIVA (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Enhantoideae; Oryzeae; Oryzea.
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein Cgl1907.
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                              Nitrosomonadaceae; Nitrosomonas
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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                                                                  NCBI_TaxID=915;
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PAFFFBBBCCCCXBBGGGGGGGGGGGG

ESULT 18

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Gaps

ESULT 19
28NPA7
1D Q8NPA
3C Q6NPA
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Best_Local Similarity 100.
Matches 4; Conservative
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297/U4
AC 097/U4;
DT 01-07T-2
DT 01-07T-2
DE HYPOCHEL
GN CACIL179.
OC CLOSTRIG
OC CLOSTRIG
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OC CLOSTRIG
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Q82MX0
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STRIN=Ssa-1, and Ssa-2;

STRIN=Ssa-1, and Ssa-2;

STRIN=S221; bubbed=12140239;

A MEDLINE=2213592; bubbed=12140239;

A Antunes A., Templecon A.R., Guyomard R., Alexandrino P.;

T genealogy of the transferrin gene in the brown trout.";

Mol. Biol. Evol. 19:127-1287 (2002).

EMBL; AF488831; AAN17017.11;

REMBL; AF488841; AAN17017.11;

REMBL; AF488841; AAN17022.1;

CO; GO:0006879; P:irrn ion binding; IEA.

GO; GO:0006879; P:irrn ion binding; IEA.

GO; GO:0006879; P:irrn ion transport; IEA.
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MEDLINE=97251358; PubMed=9097040;
MEDLINE=97251358; PubMed=9097040;
Kasai H., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
Mizobuchi K., Mori H., Mori T., Motomura K., Nakada S., Nakamura Y.,
Mashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                    Transferrin (Fragment).
Salmo salar (Atlantic salmon).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                        01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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P97252;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Late control gene D protein (Fragment).
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Pfam; PF00405; transferrin; 1.
PRINTS; PR00422; TRANSFBRRIN.
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                                                                                                                                                        PRELIMINARY;
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                                                     33 VAEF 36
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              1 VAEF 4
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QBAUPO;
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EMBL; AB07632; AAK79151.1; --
PIR; D97045; D97045.
BHYpothetical protein; Complete proteome.
SEQUENCE 74 AA; 8747 MW; 633633CB0A0C293A CRC64;
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1488;
Yamamoto Y., Horiuchi T.;
"A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392 (1996).
EMBL; D90847; BAA1549.1; -.
EMBL; D90846; BAA15938.1; -.
SEQÜENCE 72 AA; 8099 MW; 42A63B25B00EADCB CRC64;
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Bacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycineae; Streptomyces.
NCBI_TaxID=33903;
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                                                                                                                                                                                                                                                                             100.0%; Score 19; DB 2; Length 72; 100.0%; Pred. No. 1.18+03; tive 0; Mismatches 0; Indels
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SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CAC1179.
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Last annotation update)
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
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-01-JUN-2003 (TrEMBLrel. 24, Last seq.
01-JUN-2003 (TrEMBLrel. 24, Last annot Hypothetical protein.
SAVIS32.
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Hanamoto A., Takahashi C.

Ikeda H., Ishikawa J

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Van Etten J.L.;
Submitted (DEC-1995)
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                                                                                                                                                                                                                                                                                                                               MEDIANS-ZEOUSUS, TEMPREMENTO A., SHINOSE M., KIKUCHI H., SHIDA T., SAKAKI Y., ISHIKAWA J., HARDMOOLO A., SHINOSE M., KIKUCHI H., SHIDA T., SAKAKI Y., HATTOTI M., OMUTA S., "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";

Nat. Biotechnol. 21:526-531(2003).

EMBL, AR055027; BAC62943.1;

EMBL, AR055027; BAC62943.1;

EXECUTED 74 AA; 7960 NW; DSCE71C8B08AEB01 CRC64;
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidea, Bovinae, Bos.
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Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Csonce T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitiis: deducing the ability of producing secondary metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 100.0%; Score 19; DB 16; Length 74; Similarity 100.0%; Pred. No. 1.18+03; 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                     STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
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Interpro, IPR003511; DNAbind HORMA.
PROSITE; PS50815; HORMA; 1.
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SEQUENCE FROM N.A.
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962M8
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Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
De Vos W.M., Siezen R.J.,
"Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. 861. U.S.A. 100:1990-1995(2003).

Bypothatical protein; Complete protecme.
SEQUENCE 77 AA; 8618 MW; CO0E2BFFID401F2F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20013326; PubMed=10544099;
Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
Lisec A.D., Nickerson K.W., Van Etten J.L.;
"Chlorella virus PBCV-I encodes a functional homospermidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96400190; PubMed=8806566;
Kutish G.F., Li Y., Lu Z., Furuta M., Rock D.L., Van Etten J.L.;
"Analysis of 76 kb of the chlorella virus PBCV-1 330-kb genome: map
positions 182 to 258."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
NCBI_TaxID=10506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 19; DB 16; Length 77; 100.0%; Pred. No. 1.2e+03; tive 0; Mismatches 0; Indels
                                                                                      Bacteria, Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacilus.
NCBL_TaxID=1590;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                         MEDLINE=22480296; PubMed=12566566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lrology 223:303-317(1996).
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=NCIMB 8826 / WCFS1;
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Best Local Similarity 100...
4; Conservative
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                                                                         Lactobacillus plantarum.
                     Hypothetical protein.
LP_1960.
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Gaps
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EMBL; APO01514; BABG5901.1; -.

PIN; R83922; R83925.

Hypothetical protein, Complete protecome.

SEQUENCE 84 AA; 9669 MW; GCDE3768ED9F5D84 CRC64;
                                                                                                             SEGUENCE FROM N.A.
STRAIN-USDA 110;
MEDLINE=22484999;
MEDLINE=22484999;
MEDLINE=22484999;
MEDLINE=22484999;
MARCHAINE Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watenabe A., Idesawa K., Iriquchi M., Kawashina K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                        "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
BNA Res. 9:189-197(2002).
EMBL; ABO05937; BAC45927.1; -.
Complete proteome.
SEQUENCE 81 AA; 9235 MW; D512A9FFEDODA6C7 CRC64;
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STRAIN=C-125 / JCM 9153;
MEDLINEE-20512582; Pubmed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Maeui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBL_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 19; DB 16; Length 81; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 4; Conservative 0; Mismatches 0; Indels
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Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OcT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein BH2182.
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Last annotation update)
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Horikoshi K.;
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Q821D2
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Winans S.C., Zhu J., Oger P.M., Schrammeijer B., Hooykaas P.J.,
Farrand S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium tumefaciens.
Plasmid Ti.
Batceria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 79;
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100.0%; Pred. No. 1.2e+03;
ative 0; Mismatches 0; Indels
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                                                                  Van Etten J.L.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          [8]
SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Gurnon J.R., Graves M.V., Van Etten J.L.;

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, V42580; AAC96899.1; -.

PIR; T18034; T18034.

SEQUENCE 79 AA, 8698 MW; B191C627F5D5C5A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Octopine-type Ti plasmid sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF242881; AAF77180.1; -.
GO; 00046821; C:extrachromosomal DNA; IEA.
                                                                                                                                               SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 12; 100.0%; Pred. No. 1.2e+03;
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 100.v
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BSR0662.
Bradyrhizobium japonicum.
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              [6]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 VAEF 52
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Q89WL6
ID Q89WL6
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RESULT 28 Q9KI36

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MEDILINE-177867; PubMed=1848850;
Tu G.F., Achen M.G., Aldred A.R., Southwell B.R., Schreiber G.;
Tu G.F., Achen M.G., Aldred A.R., Southwell B.R., Schreiber G.;
Tu G.F., Achen M.G., Aldred A.R., Southwell B.R., Schreiber G.;
The distribution of cerebral expression of the transferrin gene is species specific.";
J. Biol. Chem. 266:6201-6208(1991).
I. Biol. Chem. 266:6201-6208(1991).
I. PUNCTION. TRANSPORT PROTEINS WHICH CAN BIND TWO APPERRING IRON BINDING OF AN ANION, USUALLY BICARBONATE.
EMBL, M64691, AAA31586.1;
PERBL, M64692; AAA31586.1;
PERBL, M38725; A38725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, koneep).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                    Stephenson S.-A., Maclean D.J., Manners J.M.;
"Disruption of a novel pathogenicity gene of Colletotrichum
gloeosporioides results in a hypersensitive response in the host
stylosanches guianensis.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 194183; AAB92222.1; -.
EMBL, 194183; AAB92222.1; -.
EMBL, 19503877; FDNA binding; IEA.
InterPro; IPR001387; HTH 3:
Pfcm; PF01381; HTH 3: 1.
Pfam; PF01381; HTH 3: 1.
Hypothetical protein.
NON TER.
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
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                                                                                                                                                                                                                                                                                                                           85 AA; 9316 MW; BFB9A0E5F44E9CF2 CRC64;
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Last annotation update)
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HSSP; P19134; ITPD.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008199; F:ferric iron binding; IEA.
GO; GO:0006879; F:ferric iron homeostasis; IEA.
GO; GO:0006826; F:iron ion transport; IEA.
InterPro; IFRO1156; Transferrin.
SWART; SWO0094; TR FER; I.
PROSITE; PSO0205; TRANSFERRIN_1: 1.
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Losite; PS0205; TRANSFERRIN.; 1.

Tron transport; Metal.binding.

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SEQUENCE 87 2 87
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A; Conserva
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                                    NCBI_TaxID=5457;
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Q99149;
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Matches
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Geng M. M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
The genome sequence of Chlamydia pneumoniae TW183 and comparison with
other Chlamydia strains based on whole genome sequence analysis.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017189; AAP98704.1;
Hypotherical protein.
SEQUENCE 84 AA; 9260 MW; 7786DF8BDD7B3AB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                   STRAIN-GPIC;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
Mindyam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
Fraser C.M.;
Fraser C.M.;
exemining the role of content of the colution of the
Chlamydiacese.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria, Chlamydiae, Chlamydiales, Chlamydiaceae, Chlamydophila.
NCBI_TaxID=83558;
Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 16; Length 84; 100.0%; Pred. No. 1.3e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 16; Length 84; 100.0%; Pred. No. 1.3e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          Hypothetical protein, Complete proteome.
SEQUENCE 84 AA; 9191 MW; 7DF6009729C7093A CRC64;
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Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25,
01-0CT-2003 (TrEMBLrel. 25,
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4; Conservative
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                                                      FROM N.A
             NCBI_TaxID=83557;
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7VPV6
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MEDITNE=93013005; PubMed=1398114;
Shih M.C., Heinrich P., Goodman H.M.;
"Cloning and chromosomal mapping of nuclear genes encoding chloroplast and cytosolic glyceraldehyde-3-phosphate-dehydrogenase from Arabidopsis thaliana.";
Gene 119:317-319(1992).
Gene 119:317-319(1992).
GOO 90009507; C:chloroplast; IEA.
                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lindler L.E., Plano G.V., Burland V., Mayhew G.F., Blattner F.R., "Complete DNA sequence and detailed analysis of the Yersinia pestis KIMS plasmid encoding murine toxin and capsular antigen."; Infect. Immun. 66:5731-5742(1998).
ENDL, AF074611, AF082761.1; -...
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                                                       Q41185;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-TUN-2003 (TrEMBLrel. 24, Last annotation update)
Glyceraldehyde-3-phosphate-dehydrogenase subunit GapB (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h Similarity 100.0%; Score 19; DB 10; Length 88; Similarity 100.0%; Pred. No. 1.38+03; 4; Conservative 0; Mismatches 0; Indels
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NON TER
SEQUENCE 88 AA; 9198 MW; FCDB6A7E37B6999D CRC64;
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Last annotation update)
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100.0%; Score 19; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0;
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                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
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NCBI_TaxID=632;
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Best Local Similarity
Matches 4; Conserv
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RESULT 37
Q41185
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"Construction of tryptophan requiring-mutant of Nitrosomonas europaea by inactivation of tryptophan using homologous recombination.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB030031; BAA83388.1;
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                                                                                                                                                                                                                                                                                                                                                                                      Hertwig S., Klein I., Schmidt V., Beck S., Hammerl J.A., Appel B., Sequence analysis of the genome of the temperate Yersinia enterocolitica phage PY54.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Bacteriophage PX54.
Viruses, dsDNA viruses, no RNA stage, Caudovirales, Siphoviridae.
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Nitrosomonadaceae, Nitrosomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hertwig S.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ564013; CAD91786.1; -.
Exonuclease; Hypothetical protein.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
Cytochrome P460 (Fragment).
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Best Local Similarity
Matches 4; Conserv
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                                                            VAEF 16
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Q9S590;
01-MAY-2000 (
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SEQUENCE
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Best Local Similarity
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Q812X3
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MEDLINE-21146866; PubMed=11248100;

May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

I "Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL; AE006066; AAX02385.1;

R HSSP; Pa00378; IAB3;

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0005640; C:ribosome; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

InterPro; IPR00125; P:structural Constituent of ribosome; IEA.

R InterPro; IPR00129; Ribosomal_S15.

InterPro; IPR00129; Ribosomal_S15.

R Prod) PD157043; RS15 bact; 1.

R PROSITS; PS00322; S15 bact; 1.

R PROSITS; PS00302; RIBOSOWAL_S15; 1.
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STRAIN=IL1403,
STRAIN=IL1403,
STRAIN=IL1403,
MEDLINA=1212316, PubMed=11337471;
BOIOtin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
The complete genome sequence of the lactic acid bacterium Lactococcus
lactis sep. lactis IL1403.";
Genome Res. 11:731-7531(2011).
BMBL, AR005385, AAK05548.1; --
BIR, P86818; P86818.
BYPOCHAELICAI protein; Complete proteome.
SEQUENCE 89 AA; 10403 MW; D90DF3CF71D12D06 CRC64;
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Bacteria; Pirmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
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Pasteurellaceae, Pasteurella.
NCBI_TaxID=747;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ypjB.
                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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RPS15 OR PM0301.
Pasteurella multocida.
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Best Local Similarity
Matches 4; Conserv
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VAEF
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01-JUN-2001
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                                                                          Gaps
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01-JUN-2001 (TERMBLEE]. 17, Created)
01-JUN-2001 (TERMBLEE]. 17, Last sequence update)
01-JUN-2003 (TERMBLEE]. 24, Last annotation update)
01-JUN-2003 (TERMBLEE]. 24, Last annotation update)
Preproinsulin (Fragment).
Ambloplites rupestris (Rock bass).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actainopterygii, Neopterygii, Teleostei, Teleostei, Euceleostei,
Centrarchidae, Ambloplites.
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AL-Mahrouki A.A., Irwin D.M., Youson J.H.;
Molecular cloning of preproinsulin cDNA from the rock bass.";
L. Submitted (OCT-1999) to the EMBL/GORDBANK/DDBJ databases.
c.i. SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
C. i. SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
R REMEL, AF199584; AAX28708.1; ...
R HSSP, PO1308; ILPH.
R GO; GO:0005179; Fhormone activity; IEA.
R GO; GO:0005179; Fhormone activity; IEA.
R GO; GO:0005179; Ins/IGF/relax.
R PERMYS; PRO0049; Ins/IGF/relax.
R PERMYS; PRO0047; INSULIN:
R PERMYS; RN00077; INSULIN:
R PRINTS; PRO0077; INSULINE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Query Match 100.0%; Score 19; DB 16; Length 89; Best Local Similarity 100.0%; Pred. No. 1.3e+03; Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yin F., Fan D.M.;
"Identifying a new variant of MADZL1.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF394735, AAN74648.1;
InterPro; IPR003511; DNAbind HORMA.
PF02301; HORMA; 1.
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SEQUENCE 90 AA; 10335 MW; 8209F5A7A7D8D09B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       QBIZX3;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MAD2 mitotic arrest deficient-like 1 variant.
MAD2L1.
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100.0%; Pred. No. 1.4e+03;
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Query Match
Best Local Similarity 100...
4; Conservative
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SEQUENCE FROM N.A.
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Q89WX7
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR313446; AAM88940.1; -.
GQ; GQ:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  046425;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 25, Last annotation update)
Aquaporin 1 (Fragment).
Aquaporin 1 (Fragment).
Divorcolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria; Lagomorpha, Leporidae, Oryctolagus.
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NCBI_TaxID=29449;
                                                                                             / Match 100.0%; Score 19; DB 13; Length 91; Local Similarity 100.0%; Pred. No. 1.46+03; les 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 2; Length 94; 100.0%; Pred. No. 1.4e+03; Ative 0; Mismatches 0; Indels
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94 AA; 10222 MW; C09D6EA3DFF1E2BA CRC64;
                                      91 91
91 AA; 10100 MW; E86C8B256DC69D39 CRC64;
                                                                                                                                                                                                                                                                                                                                        Q8KY12;
01-CCT-2002 (TrEMBLrel. 22, Created)
01-CCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UCT-2003 (TrEMBLrel. 24, Last annotation update)
Putative transcriptional regulator (Fragment).
                                                                                                                                                                                                                                                                                                                          94 AA.
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PROSITE, PS00262; INSULIN, 1.
NON_TER 1 11
NON_TER 91 91
SEQUENCE 91 AA; 10100 MW;
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Best Local Similarity 100.
Matches 4; Conservative
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SEQUENCE
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Matches 4
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MOOD D.W., Setubal J.C., Kaul R., Monke D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Ruyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Ruyavin C., Rouse G., Zaenphimmachak C., Wu Z., Romero P., Gordon D.,

Raymond C., Rouse G., S., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Nester E.W.;

"The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
VCBI_TaxID=176299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 19; DB 6; Length 94 100.0%; Pred. No. 1.4e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                          Fram; Frozzo; mr; mr; 1.
PROSITE; PS00221; MIP; family; 1.
PROSITE; PS00221; MIP; 1.
NON_TER 1 1 1
NON_TER 94 94
SEQÜENCE 94 AA; 10057 MW; 963D5527631E8CDC CRC64;
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EMBL, AB009334; AAL44840.1; -.
PIR, AB3053; AB3053.

Hypothetical protein; Complete proteome.

SEQUENCE 96 AA; 11193 MW; FBD635894846A8AE CRC64;
GO; GO:0005741; C:mitochondrial outer membrane; IEA.
GO; GO:0015289; F:porin activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000425; MIP.
Pfam; PF00230; MIP; 1.
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01-JUM-2002 (TrEMBLrel. 21, Last sequence update)
01-JUM-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atu4039.
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01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
B810551 protein.
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STRAIN=EGD-6 / Serovar 1/2a;

MEDLINE=21537279; PibMed=11679669;

MEDLINE=21537279; PibMed=11679669;

MEDLINE=21537279; PibMed=11679669;

MEDLINE=21537279; PibMed=11679669;

Medrbit A., Chetcuani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetcuani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Britan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

A Gautier I., Goebel W., Gomez-Lopez N., Hain T., Hauf U., Jackson D.,

A Madueno E., Mattournam A., Matta Vicente J., Noy E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simose N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
            Viruses, ssRNA positive-strand viruses, no DNA stage, Picornaviridae,
Hepatovirus.
NCBI_TaxID=12092;
                                                                                                                                                                                                                                                                                      "Characterization of a hepatitis A virus strain suitable for vaccine
                                                                                                                                                                          STRAIN=LSH/S;
MEDDINE=923488E3; PubMed=1668326;
MEDINE=92348BE3; Pineschi V., Prugnola A., Pellegrini V.,
Zuckerman A.J.;
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Best Local Similarity 100.0%; Score 19; DB 12; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1639;
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InterPro; IPR007138; ABM.
Pr09929; ABM; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 97 AA; 10979 MW; 9E758586E94218E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                  EMBL, 544109; AAB22740.2; -.
NON TER 97 97 AA, 10614 MW; D207F7CB93110DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
MNO25/9.
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100.0%; Pred. No. 1.5e+03;
tive 0; Mismatches 0;
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EMBL; AL591983; CAD00657.1; -.
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Matches 4; Conserv
                                                                                                                                              SEQUENCE FROM N.A
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Q8Y476;
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Q8Y476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                       STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                               "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DAR Res. 9:189-197(2002).
EMBL; AP005936; BAC45816.1;
GQ; GQ:0016020; C:membrane; IEA.
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STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;

Wriss R.B., Dunn D.M., Robb F.T., Brown J.R.;

Withe complete sequence of the Pyrococcus furiosus genome.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, AEO10262, AALS1744.1, .

Hypothetical protein; Complete proteome.

SEQUENCE 96 AA, 10804 MW; D6DAE09D096D577A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 16; Length 96; 100.0%; Pred. No. 1.4e+03; Attive 0; Mismatches 0; Indels
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100.0%; Score 19; DB 17; Length 96;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels
                            Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 AA; 10976 MW; A9E11F9AA4BC7734 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein PF1620
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UTUN-2001 (TrEMBLrel. 17, Last annotation update)
2C/3A (Fragment)
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Complete proteome.
SEQUENCE 96 AA: 10077
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Best Local Similarity
Matches 4; Conserv
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SEOUENCE FROM N.A.
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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                                                                                                                                                                                               62 VAEF 65
                                                                                                                       1 VAEF 4
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SEQUENCE
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ID 02
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MEDLINE=CONTOC 15692 / Marrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock Hadman S., Yuan Y.,
Smith K.A., Spencer D.H., Worg G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
Nature 406.959-944(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DC3000;
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.;
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
TIGR, PSPT01808; --.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
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PIR, E83244; E83244.
InterPro; IPR005545; YCII.
Pfam, PF03795; YCII.; Complete proteome.
SEQUENCE 99 AA; 10609 MW; 3AD945F44D54A85C CRC64;
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504 Mw; 62836007E4849392 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical protein.
                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PA3202.
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                                                                                     99 AA
                                                                                     PRT;
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Pfam; PF03795; YCII; 1.
Hypothetical protein; Compl
SEQUENCE 99 AA; 10504 MW
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Best Local Similarity 100..
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                                                                                     PRELIMINARY;
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Q885M3;
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Q9HZ38;
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                                              Q9HZ38
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SEQUENCE FROM N.A.

C STRAIN-ATCC 19718 / IFO 14228;

MEDLINE-22586410; PubMed-12700255,

A MEDLINE-22586410; PubMed-12700255,

A Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,

A Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;

A Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;

Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautotroph Nitrosomonas europaea.";

J. Bacteriol. 185:2759-2773 (2003).

R EMBL; BX21861; CAD85330.1;

InterPro; IPR005545; YCII.;

R Pfan; PF03795; YCII.;

Hypothetical protein; Complete proteome.

W Hypothetical protein; Complete proteome.
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STRAIN=ATCC 55739;
Nam 8.J., Kim J.H.;
Nam 8.J., Kim J.K.;
Nam 8.J., Kim J.K.;
Nam 8.J., Kim J.K.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF401482; AA460142.1;
GO; GO:0003746; F:Lranslation elongation factor activity; IEA.
GO; GO:0003746; F:Lranslational elongation; IEA.
InterPro; IPR001816; EF IS.
Pfam: PF00889; EF IS.
                                         Gaps
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Similarity 100.0%; Pred. No. 1.5e+03;
4; Conservative 0; Mismatches 0; Indels
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Lactobacillus reuteri.
Lactobacillus.
Lactobacillus.
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Last annotation update)
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Q8VS54;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
Elongation factor TS (Fragment).
                Pred. No. 1.5e+03;
Mismatches 0;
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100.0%; PIT
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01-UNM-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
HYPOChetical protein.
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SEQUENCE FROM N.A.
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NON TER
SEQUENCE 10
                                                  Fraser C.M.;
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Q7Z2N2;
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Q9F368
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CATAIN=ATCC 35092 / DSM 1617 / P2;

STRANN=ATCC 35092 / DSM 1617 / P2;

MEDLINE=2133236; PubMed=11427726;

A She Q., Singh R.K., Confalonier'F., Zivanovic Y., Allard G.,

A Awayez M.J. Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

EMBL; H90297; H90399; JUF196.

R Pfam, PF02647; DUF196; 1.
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                                                                                                                                                                                                                                         Archaea, Crenarchaeota, Thermoprotei, Sulfolobales, Sulfolobaceae, Sulfolobus.
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100.0%; Score 19; DB 2; Length 101; 100.0%; Pred. No. 1.5e+03; Live 0; Mismatches 0; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TaxID=198094;
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Hypothetical protein; Complete proteome.
SEQUENCE 101 AA; 11936 MW; A7C338AD76202E17 CRC64;
                                                                                                                                         097YC2 PRELIMINARY, PRT, 101 AA. 097YC2, 010-0CT-2001 (TEWBLrel. 18, Created) 01-0CT-2001 (TEWBLrel. 18, Last sequence update) 01-UTW-2003 (TEWBLrel. 24, Last annotation update) Hypothetical protein SSO1404.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
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  Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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                                                                           62 VARF 65
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Q81R27,
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Matches
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Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Warkins K.L., Nierman W.C.,
Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
BKISOC2.6 (Putative novel protein similar to APOBECI (Apolipoprotein BKISOC2.6 (Putative novel protein) (Fragment).
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                                                                                                                                     "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
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Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                 Length 102;
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103 103
103 AA; 12146 MW; 5DC969AB3ED34BD9 CRC64;
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SEQUENCE 102 AA; 11925 MW; 13B8E296C8A341B1 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SCO4420.
SCO4420 OR SC6F11.18.
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100.0%; Pred. No. 1.5e+03;
iive 0; Mismatches 0;
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                                                                                                                                                                                                   Nature 423:81-86(2003).
EMBL; AE017031; AAP26109.1; -.
TIGR; BA2232; -.
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Best Local Similarity 100.
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Matches 4; Conservative
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STRAIN=GB-MI;
MEDLINB=21576510; PubMed=11719806;
Katinks=21576510; PubMed=11719806;
Katinks M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
Weissenbach J., Vivares C.P.;
Weissenbach Gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
Nature 414:450-453[2001].
BMBL, ALS99445; CAD26596.1; -.
Hypothetical protein.
SEQUENCE 105 AA; 11897 MW; 08059108C05D3BB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Encephalitozoon cuniculi.
Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI_TaxID=6035;
                                                         Pedulla M.L., Ford M.E., Hourz J.M., Karthikeyan T., Wadsworth C Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R., Brucker W., Kumar V., Kandasawy J., Keenan L., Bardarov S., Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W., Hatfull G.F., Camillians of highly mosaic mycobacteriophage genomes."; Cell 113:171-182(2003) AAN02111.1; -- EMBL, AXI29339; AAN02111.1; -- SEQUENCE 104 AA, 11074 MW; BBB06EBAC401E9FD0 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ECU05_0770.
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01-JUN-2003 (TrEWBLrel. 24, Last sequence update)
01-JUN-2003 (TrEWBLrel. 24, Last annotation update)
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                                MEDLINE=22592660; PubMed=12705866;
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Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., (Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Exbbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
BNA Res. 9:189-197(2002).
EMBL; AP005950; BAC49378.1; -.
Complete proteome.
SEQUENCE 103 AA; 11104 MW; BF27CB9F90FBB723 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=205880;
[1]
                                                                                                                                                                                                                                      Hopwood D.A.;

"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";

Nature 417:141-147(2002).

EMBL, A1939120, CAC08429.1; -.

Hypothetical protein; Complete proteome.

SQUENCE 103 AA; 11387 MW; 55C2B80589EB75B5 CRC64;
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Matches 4; Conservative 0; Mismatches 0; Indels
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Bradyrhizobium japonicum.
Bracteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Q856B5;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Gp57.
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
Blr4113 protein.
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=205875;
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Query Match 100.0%; Score 19; DB 5; Length 105; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 4; Conservative 0; Mismatches 0; Indels
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STRAIN=LL;
MEDLINE=97146421, PubMed=8990309;
MEDLINE=971464222, PubMed=8990309;
MESSIGNE P.S., McLarnan J., Leigh J.A.;
McSenase phylogeny and the molybdenum dependence of nitrogen fixation in Methanococcus maripaludis.";
J. Bacteriol. 179:541-543(1997).
EMBL; U75887; AACG5519.1;
PIR; T10097; T10097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 1; Length 106; 100.0%; Pred. No. 1.6e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                 STRAIN=LL;
BUELINE=96011360; PubMed=7592322;
Blank C.E., Kessler P.S., Leigh J.A.;
"Genetics in methanogens: transposon insertion mutagenesis methanococcus maripaludis nifH gene.";
J. Bacteriol. 177:5773-5777(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003731; DUP153.
Pfam; PF02579; Nitro FeMo-Co; 1.
SEQUENCE 106 AA; I1862 MW; 4734D89CFED33F3B CRC64;
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanococcaceae; Methanococcus.
NCBI_TaxID=39152;
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Q9BGL5
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C STRAIN=JCM 10545 / 7;

K MEDLINE=J456156; PubMed=11572479;

K RAWATabayael Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

A Sekine M., Baba S.-I., Ahkai A., Kosugi H., Fosyama A., Fukui S.,

A Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

Noshizawa T., Tanaka T., Xudohi Y., Yamazaki J., Kushida N., Oguchi A., Poshia T., Kikuchi H.;

A Okiia T., Kikuchi H.;

Complete genome sequence of an aerobic thermoacidophilic

T Complete genome sequence of an aerobic thermoacidophilic

T Crenarchaeon, Sulfolobus tokodaii strain? ";

DNA Res 8.123-140(2001)

E EMB1, AP000988 BAB67095.1; -.

R FAB1, AP000988 Transposase_29.

R Pfam; PRO4693; Transposase_29.
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                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

PEDLINE-22552660, PubMed=12705866;

Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,

Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzto N.R.,

Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,

Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,

Harfull G.F.,

Coll 113:171-182(2003)

EMBL, X129335, AAN01935.1;

SEQUENCE 105 AA, 11955 MW; 7DOEC09F5F2AF2DD CRC64;
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100.0%; Score 19; DB 17; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
NTPOCHETICAL Protein ST2000.
ST2000.
Sulfolobus tokodaii.
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Best Local Similarity 100.
Matches 4; Conservative
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P71530;
01-FEB-1997 (
01-FEB-1997 (
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$9BGL5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Matrilysin (Fragment).
Ovis aries (Sheep).
Eukaryotes, Metacos, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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Suith G.W., Ricke W.A., Cassar C.A., Smith M.F.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF267158; AAG59846.1;
RISSP; P09237; 11WMO.
RMEOPS; M10.008;
MEOPS; M10.008;
Co; G0:0005508; C:extracellular matrix; IEA.
GO; G0:000522; F:metalloendopeptidase activity; IEA.
GO; G0:0005508; P:proteolygis and peptidolysis; IEA.
RICHEPPO; IPRO01818; Peptidase M.
RICHEPPO; IPRO01818; Peptidase M.
RICHEPPO; IPRO01818; Peptidase M.
REAM; PR001318; MATRIXIN.
REMINTS; EM00235; ZNMC; 1.
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Length 107;

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100.0%; Score 19; DB 3; I
100.0%; Pred. No. 1.6e+03;
                                                                                 0; Mismatches
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Query Match
Best Local Similarity 100..
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SEQUENCE FROM N.A.
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QBNRX6
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QBIHV3
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MEDLINE=21135672; PubMed=11238395;
Bean L.E., Dvorachek W.H. Jr., Braun E.L., Errett A., Saenz G.S.,
Giles M.D., Werner Washburne M., Nolson M.A., Natvig D.O.;
"Analysis of the pdx-1 (snz-1/sno-1) region of the Neurospora crassa genome. Correlation of pyridoxine-regulring phenotypes with mutations
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DAN-1998 (TrEMBLrel. 19, Last annotation update)
01-DEC-2010 (TrEMBLrel. 19, Last annotation update)
Cathepsin B-like cysteine proteinase (Fragment).
77123-13.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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Genetics 15:1067-1075(2001).
EMBL; AF30068; AAK07845.1;
HSSP; P80028; 170F.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005118; P:electron transport. IEA.
InterPro; IPR006662; Thiored.
InterPro; IPR006663; Thiored.
Pfam; PF00085; Thioredy 1.
PRINTS; PR00421; THIOREDOXIN.
Redox-active center.
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107 AA; 11676 MW; CF4E6EAF85BE3776 CRC64;
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01-JUN-2001 (TrEMBirel. 17, Last sequence update)
01-JUN-2003 (TrEMBirel. 24, Last annotation update)
Putative thioredoxin G6G8.7.
                                                                                                                                                                     106 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
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                                                                                                                                                            023682;
023682;
01-JAN-1998 (
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023682
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EMBL; AP005276; BAB99308.1; -.
InterPro; IPR007138; ABM.
Pfam; PF03992; ABM; 1.
Complete proteome.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCB_TaxID=36329;
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100.0%; Pred. No. 1.6e+03;
tive 0; Mismatches 0; Indels
Indels
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Nature 419:499-511(2002).
EMBL ABO14842. AAN36006.1; -.
Hypotherical protein.
SEQUENCE 107 AA; 12714 MW; CA351258FCF46EF5 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Uncharacterized ACR.
                                                                                                                                                                                                                                                                                                                             01-WAR-2003 (TrEMBLrel. 23, Created)
1-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
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Query Match
Best Local Similarity 100..
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Q7TX28;
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Q7TX28
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Deviln K., Fellwell T., Gentles S., Hamin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
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MEDLINE-2002293; PubMed=10555283;

Hughes S., Zelus D., Mouchiroud D.;

Hughes S., Zelus D., Mouchiroud D.;

Mol. Biol. Evol. 16:1521-1527(1999).

EMBL, AJO11392; CAB56418.1; -..

R GO; GO:0005215; F:transporter activity; IEA.

R GO; GO:00056810; P:transporter activity; IEA.

R GO; GO:0005691; P:transporter activity; IEA.

R GO; GO:0005691; P:transporter activity; IEA.

R HOSP: PRO0215; F:transporter activity; IEA.

R HOSP: PRO0216; F:transporter activity; IEA.

R Fam; PF00061; Iipocalin.

R PRINTS; PR0179; LIPOCALIN.

R PRINTS; PR0179; LIPOCALIN.

T NON TER 109 AA; 12552 MW; ODCAB93895B91A23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUM-2003 (TrEMBLrel. 24, Last annotation update)
Retinol binding protein (Fragment).
Crocodylus niloticus (Rile crocodile) (African crocodile).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Archosauria, Crocodylidae; Crocodylinae; Crocodylus.
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                                   h 100.0%; Score 19; DB 16; Length 107; Similarity 100.0%; Pred. No. 1.6e+03; 4; Conservative 0; Mismatches 0; Indels 0
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107 AA; 12373 MW; B5ACF23621078018 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Rv3183.
Rv3183 OR MTV014.27 OR MT3275.
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3Q SEQUENCE
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STRAIN-CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann K.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Deloher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Rroc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
Complete protecome.

Complete protecome.
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"Whole genome comparison of Mycobacterium tuberculosis clinical and
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544 (1998).
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Bacteria, Actinobacteridae, Actinomycetales, Corymebacterineae, Mycobacteriaceae, Mycobacterium.
Corymebacterineae, Mycobacteriaceae, Mycobacterium.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021646; CAA16648.1; -.
EMBL; AS007140; AAK47615.1; -.
PIR; E70949; TF0949.
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SWART; SM00530; HTH XRE; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 109 AA; 11802 MW; A66DBE160D79613A CRC64;
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01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last amnotation update)
Possible transcriptional regulatory protein.
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MEDLINE=22709107; PubMed=12788972;
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                         73 VAEF 76
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1 VAEF 4
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Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
A Random DNA Sequencing, Computer-Based Approach for the Generation
of a Gene Map of Molluscum Contagiosum Virus.";
Virus Genes 0:0-0(1997).
EMBL, US6919; AABS7977.1; -.
NON TER 10 110
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Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Foute D.E., Gill S.R., Pop M., Helmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Hein S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                   01-JTL-1997 (TrEMBLrel. 04, Created)
01-JTL-1997 (TrEMBLrel. 04, Last sequence update)
01-JTL-1997 (TrEMBLrel. 04, Last sequence update)
X1-1900 (TrEMBLrel. 19, Last annotation update)
X1-5 protein (Fragment).
X1-6 protein (Fragment).
X1-7 protei
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBL_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 12; Length 110; 100.0%; Pred. No. 1.6e+03;
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100.0%; Score 19; DB 16; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
EMBL; AEOLG790; AAN70076.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 110 AA; 11856 MW; 6AE9CE25FC3DB780 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
YCII-related domain protein.
                                              110 AA
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Pfam, PP03795; YCII; 1.
Complete proteome.
SEQUENCE 110 AA; 11775 M
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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                              STRAINSTOIL / DSM 3638 / ATCC 43587 / JCM 8422;
Wheis R.B., Dunn D.M., Robb P.T., Brown J.R.;
Wheis R.B., Dunn D.M., Robb P.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMEL, ABC10208; AALG1067.1;
InterPro: IPRO/342; HEBN.
Pfam, PRO5168; DUF712; 1.
PHYDOCHELICAL PROCEED: Complete proteome.
Hypothetical protein; Complete proteome.
SEQUENCE 111 AA: 13379 MW; C6A005A6E2B6CAAE CRC64;
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Best Local Similarity 100.0%; Pred, No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY204162; AY039166.1;
4GD; GO:0004872; F:receptor activity; IEA.
InterPro; IPR008946; Str_ncl_receptor
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                                       01-UN-2002 (TrEMBLrel. 21, Created)
01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PF0943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Nuclear receptor NHR-1 (Fragment).
Caenorhabditis elegans.
111 AA
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VAEF 4
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Sequence 3
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APPLICANT: Doane, Minh Tam
APPLICANT: Doane, Minh Tam
APPLICANT: Doane, Minh Tam
APPLICANT: Doane, Minh Tam
APPLICANT: John, Varghese
APPLICANT: Trigon, No. 6627739mand
APPLICANT: Tatsuno, Gwen
APPLICANT: Tatsuno, Gwen
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Tung, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: WANGER: US/09/724,566A
CURRENT FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-06-15
NUMBER: OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 78
LIBNICH: WANGER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 19; DB 4; Length 7; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
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; LOCATION: 3
; OTHER INFORMATION: Xaa is hydroxyethylene or statine US-09-724-566A-78
                                                                                                US-09-252-991N-23529
US-09-053-702-2
US-09-053-702-2
US-09-372-420A-8
US-09-3172-440A-4
US-09-314-701-30
US-09-314-701-30
US-09-314-701-30
US-09-372-420A-18
US-09-372-420A-18
US-09-372-420A-18
US-09-372-420A-14
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
                                                    9-489-039A-9313
9-489-039A-12815
9-252-991A-23529
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Gurigbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Fower, Michael
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 78, Application US/09724566A Patent No. 6627739
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Best Local Similarity
Matches 4; Conserv
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PEBULT 2 - Sed. 81

US-07-124-Sed. 82

US-07-124-Sed. 82

US-07-124-Sed. 82

US-07-124-Sed. 83

US-07-124-Se
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Patentin Release #1.0, Version #1.25
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Best Local Similarity 100.
Matches 4; Conservative
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STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Power, Michael
Sinha, Sukanto
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MOLECULE TYPE: peptide
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Sequence 145
Sequence 145, Application US/08197484
Patent No. 6419931
GENERAL INFORMATION:
APPLICANT: UTILELLO, Maria A.
APPLICANT: SETTE, Alessandro D.
APPLICANT: CELIS, Esteban
APPLICANT: CELIS, Bateban
APPLICANT: GELIS, Housendro D.
APPLICANT: CELIS, Esteban
APPLICANT: CELIS, Esteban
APPLICANT: CELIS, Housendro D.
APPLICANT: CELIS, Esteban
APPLICANT: CELIS, ESTEBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Bloppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Bloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAETENIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION NUMBER: US 07/935,811
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: US 07/874,491
FILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: US 07/877,682
FILING DATE: 29-ANN-1992
PRIOR APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: PARMELOATION NUMBER: 31-300
REFERENCES/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEFHONE: (206) 623-6793
INFORMATION POR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
LENGTH: 9 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 4; Conservative
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            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: un
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Gaps
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APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OP INVENTION: Methods
TITLE OP INVENTION: Methods
TITLE OP INVENTION: Methods
TITLE OP INVENTION: Methods
TITLE OP INVENTION: MOUBER: US/09/724,566A
CURRENT APPLICATION NUMBER: US 09/501,708
PRIOR APPLICATION NUMBER: G0/119,71
PRIOR PILING DATE: 1099-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/119,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 4; Length 9; 100.0%; Pred. No. 3e+05;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 428
CLASSIFICATION: 428
APPLICATION: DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: 108 07/749,568
APPLICATION NUMBER: 31,990
RECISTRATION NUMBER: 31,990
RECISTRATION NUMBER: 31,990
REPERRNCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 467-9600
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERIFFICS:
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APPLICANT: Basi, Guriqbal
APPLICANT: Boane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
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TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide
PCT-US95-02121-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VAEF 4
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                                                                                                                                                                             PCT-US95-02121-145
                                                                                                                                RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 19; DB 5; Length 9; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 19; DB 4; Length 9; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 86, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELJ
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READBABE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DAYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PTITNE NAME: 1 - TOTAL INC.
FILED TO THE POSITION TO THE POSITION
                                                                                                                                OTHER INFORMATION: P4-P4'staD-V peptide inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NOUSEST CLASSIFICATION DATE: 16-FEB-1995
CLASSIFICATION THE STATE OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                     VUMBER: PCT/US95/02121
16-FEB-1995
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
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STRANDEDNESS: un
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PCT-US95-02121-86
                                                                                                                                                                             FEATURE:
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RESULT 7

RESULT 7

RESULT 7

RESULT 145

Sequence 145, Application PC/TUSS502121

SEQUENCE 145, Application PC/TUSS502121

REPLOCHTUSE NOWARTHON TO THE NUMBER OF SEQUENCES 133

NUMBER OF SEQUENCES 133

CONDUTER REALISE PORM:

CONDUCER REPRESENCE PORM:

CONDUTER REALISE PORM:

CONDUCER PORM:

CONDUCER
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APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: WacConlogue. Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: WANGER: US/09/724,566A
CURRENT APPLICATION NUMBER: US/09/724,566A
PRIOR FILING DATE: 2000-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 97
LENGTH: 14
APPLICANT: Angle Shuwen
APPLICANT: Wang Shuwen
APPLICANT: Wang Shuwen
APPLICANT: Wang Shuwen
APPLICANT: McConloque, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR PILING DATE: 2000-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR PLICATION NUMBER: 60/119,77
PRIOR PLICATION NUMBER: 60/139,172
PRIOR PLICATION NUMBER: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SEQ ID NO 72
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 4; Length 14; 100.0%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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OTHER INFORMATION: APP-derived fragment P10-P4' (D-V)
IS-09-724-566A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: P10-P4'staD-V peptide inhibitor
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NAME/KEY: MOD_RES
LOCATION: 10
CTHER INFORMATION: Xaa is statine moiety
3-09-724-566A-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Anderson, John P.
APPLICANT: Basi, Guridpal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Pohn, Varignese
APPLICANT: Power, Michael
APPLICANT: Sona, Sukanto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 97, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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; Sequence 3. Application US/08733825
; Patent No. 5873839
; GENERAL INFORMATION:
APPLICANT: Toth, Matthew J.
APPLICANT: Most J.
COUNTER: O. 5837839artis Patent and Trademark Department STREET: 59 Route 10
CITY: East Hamover J.
STREET: SP Route 10
CONNTRY: USA
ZIP: Read-ABLE FORM:
MEDIVER READ-ABLE FORM:
MEDIVER READ-ABLE FORM:
MEDIVER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Percentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,825
FILING DATE: 18-OCT-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 4-20615/P1/CGC 1834
TELEGONMUNICATION NUMBER: 4-20615/P1/CGC 1834
TELEGONMUNICATION NUMBER: 4-20615/P1/CGC 1834
TELEGONMUNICATERISTICS:
TELEFAX: (908) 277-510
TELEFAX: (908) 277-510
TELEFAX: (108) 277-5406
INPORMATION FOR SEQ ID NO: 3:
INMOTHER INFORMATION:
INFORMATION POR SEQ ID NO: 3:
INMOTHER INFORMATION:
INFORMATION POR SEQ ID NO: 3:
INMOTHER INFORMATION:
INMOTHER I
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100.0%; Score 19; DB 4; Length 14; 100.0%; Pred. No. 48;
                                                                            0; Mismatches
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Patent No. 5708149

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena

APPLICANT: Harkness, Robin

APPLICANT: Schryvese, Anthony

APPLICANT: Chong, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not relevant
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       Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                             11 VAEF 14
                                                                                                                                                1 VAEF 4
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US-08-487-890A-69
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US-08-39-99-6A-1

Sequence 1, Application US/08393996A
Patent No. 5858702
GENERAL INFORMATION:
APPLICANT: Agre, Peter C.
TITLE OF INVENTION: Isolation, Cloning and Expression of TITLE OF INVENTION: Transmembrane Water Channel Proteins NUMBER OF SEQUENCE: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STREET: 1001 G Street, N.W.
COUNTRY: US
ZIP: 20001
COUNTRY: US
ZIP: ADDRESSES: PALENTIN RC-DOS/MS-DOS
SOFTWARE: PALENTIN RC-BOS/MS-DOS
SOFTWARE: PALENTIN RC-BOS/MS-DOS
SOFTWARE: PALENTIN RC-BOS/MS-DOS
SOFTWARE: PALENTIN RC-BOS/MS-DOS
SOFTWARE: PALENTIN RC-BOS NOS-DOS
SOFTWARE: AFFER-USS
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 1107.48633
TELEPRAN: 202 508-9100
TELEPRAN: 202 508-9100
TELEPRAN: 202 508-9100
TELEPRAN: 202 508-9100
TELEPRAN: AFFER-USS
TELEPRAN: 202 508-9100
TELEPRAN: AFFER-USS
TELEPRAN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                  PRIOR APPLICATION NUMBER: US/08/468,763
FILING DATE: 06-UUN-1995
CLASSIFICATION: 40-000-1995
FRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/393,996
FILING DATE: 24-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: POSOTORE, LAURENCH H.
REGISTRATION NUMBER: 34-698
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 10 No: 1:
SEQUENCE CHARACTERISTICS:
LINGTH : 35-amino acids
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Best Local Similarity 100.
Matches 4; Conservative
TURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-763-1
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STRANDEDNESS: si
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STRANDEDNESS: si
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; Sequence 1, Application US/08468763
; Parent No. 5741671
; CARREAL INFORMATION:
; TITLE OF INVENTION: Isolation, Cloning and Expression of TITLE OF INVENTION: Transmembrane Water Channel Proteins; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegrett;
CTPY: Washington, D.C.
STATE: D.C.
STATE: D.C.
COUTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 1; Length 35; 100.0%; Pred. No. 1.3e+02;
                      APPLICANT: Margin, Andrew
APPLICANT: Wardin, Andrew
APPLICANT: Wardin, Andrew
APPLICANT: Wardin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSE: Sim & McBurney
STREET: 6th Floor, 330 Unviersity Avenue
CITY: Toronto
CONTRY: Canada
ZIP: MAG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC Compatible
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: BAFOC COMPATIBLE
COMPUTER: DEFLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-UN-1993
CLASSITCATION: 435
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
RRICK APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
RRICK APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATPLICATION NUMBER: US 08/148,968
FILING APPLICATION NUMBER: US 08/148,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REPERENCE/DOCKET NUMBER: 1038-466 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPRONE: (416) 595-1163
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0, Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   Gray-Owen, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
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US-08-487-890A-69
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US-08-468-763-1
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US-08-337-483-69
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US-08-478-373-69
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
Length 35;
                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHENEAL INCOMPATION:
CHENEAL INCOMPATION:
APPLICANT: LOOSMORE, Robin
APPLICANT: GARY-YORE, ALCHONY
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Mardin, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STREET: Suite 701, 330 University Avenue
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STREET: Suite 701, 330 University Avenue
S
100.0%; Score 19; DB 2; I 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1038-462 MIS:vg
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY AGENT: INFORMATION:
AMONE OF ATTORNEY AGENT.
                                                                                                                                                                                                                                                                                                                                                           ESULT 14
S-08-478-435-69
Sequence 69, Application US/08478435
Patent No. 592323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REPRENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                        14 VAEF 17
                                                                                                                                                        1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
S-08-478-435-69
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US-89-137-483-69

PREMENT NO. 5232565

PREMENT SCHAPPER, Anthony
APPLICANT: CARY-Over, Scott
APPLICANT: CARY-Over, Scott
APPLICANT: Maddy Nat-Ping
APPLICANT: Maddy Nat-
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14 VAEF 17
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US-08-474-671-69
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100.0%; Score 19; DB 2; Length 35;
Best Local Similarity 100.0%; Fred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/478,37
FILING DATE: 08-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/37,483
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 08-NOV-1993
ATPORNEY/AGENT INFORMATION:
ANAMER: MACHAEL
ANAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LOSEMOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Harkness, Robin
APPLICANT: Ghong, Pen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Wang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 24,973
REPERENCE/DOCKET NUMBER: 1038-463 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
INFORMATION POR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 69, Application US/08474671 Patent No. 6008326
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-478-373-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 17
US-08-474-671-69
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14 VAEF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 19; DB 3; Length 35; 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESULT 19
S-08-897-438-69
Sequence 69, Application US/08897438
Sequence 69, Application US/08897438
Patent No. 6262016
GENERAL INCORMATION:
APPLICANT: Locsmore, Sheena
APPLICANT: Gray-Oven, Soct
APPLICANT: Gray-Oven, Soct
APPLICANT: Yang, Van-Ping
APPLICANT: Yang, Van-Ping
APPLICANT: Wirdin, Andrew
APPLICANT: Wirdin, Andrew
APPLICANT: Wirdin, Andrew
APPLICANT: Klein, Michel
APPLICANT: Klein, Michel
APPLICANT: Mirdin, Andrew
APPLICANT: Klein, Michel
APPLICANT: Andrew
APPLICANT: Mirdin, Andrew
APPLICANT: Andrew
APPLICANT: Mirdin, Andrew
APPLICANT: Mirdin, Andrew
APPLICANT: Andrew
APPLICANT: Mirdin, Andrew
APPLICANT: Andrew
APPLICANT: STREET: Granda
ZIP: MAGG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREPLICATION NUMBER: US/08/897,438
FILING DATE:
CLARRENT APPLICATION NUMBER: US/08/897,438
FILING DATE:
CLARRENT APPLICATION NUMBER: US/08/897,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/175,116

FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/148,968

FILING DATE: 08-NOV-1993

ATOMES'AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REPERENCE/DOCKET NUMBER: 1038-511

TELEPHONE: (416) 595-1153

INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/483,577
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VAEF 4
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S-08-483-577A-69
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PETING DEAL OR-NOTION:

NAME: SCREAT, MACHAEL I

NAME: SCREAT, MACHAEL
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1 VAEF 4
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100.0%; Score 19; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
   Length 35;
Query Match 100.0%; Score 19; DB 4; Length 35 Best Local Similarity 100.0%; Pred. No. 1.38+02; Matches 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6th Floor, 330 Unviersity Avenue CITY: Toronto STATE: Ottoaria COUNTRY: Canada ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentln Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/649,518 FLING DATE: 17-MAY-1996 CLASSIFICATION NUMBER: US/08/649,518 FLING APPLICATION NUMBER: US/08/48,577 FLING APPLICATION NUMBER: US/08/48,577 FILING DATE: 07-JUN-1995 FILING DATE: 07-JUN-1995 FILING DATE: 07-JUN-1995 FILING DATE: 07-JUN-1995 FILING DATE: 29-DEC-1993 FILING DATE: 29-DEC-1993 ATTORNEY/AGENT INFORMATION: MACHAEL MACHAIN NUMBER: US/08/148,968 FILING DATE: 08-NOV-1993 ATTORNEY/AGENT INFORMATION: TELEPRATION NUMBER: 24,973 REFERENCE/DOCKET NUMBER: 1038-608 TELEPRATICATION NUMBER: 24,973 REFERENCE/DOCKET NUMBER: 1038-608 TELEPRATICATION NUMBER: 24,973 REFERENCE/COCKET NUMBER: 24,973 REFERENCE/COCKET NUMBER: 1038-608 TELEPRATICATION NUMBER: 255-1165 TELEPRATICATION NUMBER: 255-1165 TELEPRATICATION NUMBER: 24,973 REFERENCE/COCKET NUMBER: 1038-608 TELEPRATICATION NUMBER: 24,973 REFERENCE/COCKET NUMBER: 1038-608 TELEPRATICATION NUMBER: 1008-608 TELEPRATICATION NUMBER: 24,973 REFERENCE/COCKET NUMBER: 1038-608 TELEPRATICATION NUMBER: 255-1163 INFORMATION FOR SEQUIDOUS (416) 595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LOOSMORE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 Unviersity Avenue
                                                                                                                                                                                                                                                                                                                                                 Sequence 69, Application US/08649518
Patent No. 6361779
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 35 amino acids
amino acid
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                                                                                                                                1 VAEF 4
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GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT PEPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13555

LENGTH: 69
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US-05-39-39-34-80

Sequence 80, Application US/09393634

Fatent No. 6558910

SERVERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
ITILE REFERENCE: 02307E-098000US
FILE REFERENCE: 02307E-098000US
CURRENT APPLICATION NOMBER: US/09/393,634

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 92

SEQ ID NO 80

LENGTH: 68

LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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ilarity 100.0%; Pred. No. 2.6e+02;
Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.5e+02
Matches 4; Conservative 0; Mismatches 0
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US-09-328-352-7111
; Sequence 7111, Application US/09328352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: human GR24
US-09-393-634-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
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Sequence 1412, Application US/09732210
; Patent No. 673361
; GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Bunkers, Cindy A.
APPLICANT: Mittanck, Cindy A.
APPLICANT: Weltenck, Cindy A.
FILE REFERENCE: 38-21(15036)
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 4; Length 74; 100.0%; Pred. No. 2.8e+02; ive 0; Mismatches 0; Indels
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ALDRESSE:

ALINGTON

STREET:

ARLINGTON

CITY:
ARLINGTON

COUNTRY:

ALINGTON

ZIP:
22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE:
FORM:
MEDIUM TYPE:
FORM:
MEDIUM TYPE:
FORM:
MEDIUM TYPE:
FORM:
COMPUTER:
FORM:
MEDIUM TYPE:
MEDIUM TANGRES:
MILSON

REGISTRATION NUMBER:
MARY J.
REGISTRATION NUMBER:
TELEPHONE:
MARY:
TELEPHONE:
MARY J.
MEDIUM TOR SEQ ID NO:
MED
                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08894139
Fatent No. 6448376
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: LA THANGUE, RENE
APPLICANT: HITMANDS, BLEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF ESQUENCES: 25
CARRESPONDENCE ADDRESSE:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                               47 VAEF 50
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US-08-894-139-10
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                                                                                                                       셤
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: GTOS9-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEG ID NO 7111
LENGTH: 71
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Sequence 10. Application US/08321071A
Patent No. 5672666
GENERAL INFORMATION:
APPLICANT: CHITTENDEM, Thomas D.
APPLICANT: CHITTENDEM, Thomas D.
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCES: 31
CORRESPONDENCES: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STRIE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US9410103
FILING DATE: 11-OCT-1994
CLASSIFICATION NUMBER: PCT/US95/10103
FILING DATE: 100-AUG-1995
PRIOR APPLICATION NUMBER: 09-AUG-1995
FILING DATE: 109-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 109-AUG-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 202-942-8484
TELECOMMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOM
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100.0%; Score 19; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 19; DB 4; L
100.0%; Pred. No. 2.6e+02;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Acinetobacter baumannii IS-09-328-352-7111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 73 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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MOLECULE TYPE: peptide
IS-08-321-071A-10
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                      Query Match
100.0%; Score 19; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SUSTING SYSTEM: PC-DOS/MS-DOS
SUSTING PATE: 19901114
CLASSIFICATION NUMBER: US/07/612,674
FILING DATE: 19901114
CLASSIFICATION: ATSON T.
REGISTRATION: WATSON T.
REGISTRATION NUMBER: 5683/82332
TELEFOND: 202-861-3027
TELEFOND: 202-861-3027
TELEFOND: 202-861-3027
TELEFOND: 202-861-3027
TELEFOND: SEQ ID NO: 12:
LENGTH: 93 amino acids
LENGTH: 93 amino acids
STERANDERSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: NUELL, MARK J. APPLICANT: MCLUNG, J. KEITH
APPLICANT: STEWART, DAVID A.
APPLICANT: DANNER, DAVID B.
TITLE OF INVENTION: AN ANTIPROLIFERATIVE PROTEIN
NUMBER OF SEQUENCES: 14
CORRESSEDNUENCE ADDRESS:
ADDRESSEDE: CUSHMAN, DARRY & CUSHWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CUSHWAN, DARBY & CUSHWAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA
PRIOR APPLICATION NUMBER: US 60/169,340 PRIOR FILING DATE: 1999-12-07 UNDBER OF SEQ ID NOS: 1753 SEQ ID NO 1412 LENGTH: 88
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/07612674
Patent No. 5658792
                                                                                                           ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-732-210-1412
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Best Local Similarity 100.
Matches 4; Conservative
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RESULT 29 US-09-543-681A-5816

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ZIP: 02109
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                                                                                                                                    Gaps
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Sequence 8, Application US/08246361A
Patent No. 599582
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
ADDRESSE: LAHVVE & COCKFIELD
STREST: 60 State Street
CITY: Boston
CITY: Boston
CITY: MA
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                                                         100.0%; Score 19; DB 2; Length 100; 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFACATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/886,178
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATE: 45-MAY-1992
PRIOR APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNAY JAGENT INFORMATION:
NAME: Matthew P. Vincent
RECISTRATION NUMBER: 36,709
REFERENCE-DOCKET NUMBER: 36,709
REFERENCE-DOCKET NUMBER: 36,709
REFERENCE-DOCKET NUMBER: A6,709
REFERENCE-DOCKET NUMBER: A6
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                    4; Conservative
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                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                 13 VAEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 VAEF 16
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S-08-464-517-8
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Sequence 8, Application US/08463772 Patent No. 6066501

ESULT 32 IS-08-463-772-8

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CONTINGENT NEARLY SHOWS BACKED SAIGH.

APPLICATION BRANETON: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEGURACES: 50
COMESSONECE ADDRESS: 50
COMESSONECE ADDRESS: 50
CONTINGENT BACKED.
STREET: 60
STREET:
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us-09-594-978a-2.rai

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DESCRIPTION: protein POTHETICAL: no
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Patent No. 5856161
GENERAL INFORMATION:
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: Adder
STREET: BOIL Candle Lane
STREET: BOIL Candle Lane
CITY: Houston
STREET: Texas
COUNTRY: USA
ZIP: 77071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 19; DB 5; Length 100; Best Local Similarity 100.0%; Pred. No. 3.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
TELECHONEICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER FEADABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
PLILOGIATION NUMBER: US/08/580,988A
FILLING DATE: January 3, 1996
                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 25-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMENICATION INFORMATION:
TELECOMENICATION INFORMATION:
TELECOMENICATION INFORMATION:
TELECOMENICATION INFORMATION:
TELECOMENICATION OF 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
     APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 21:
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                                                                                                                                                                                                                                                                                                                                                                                                     / UNDECTUB TYPE: protein PCT-US93-05000-8
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                               FILING DATE: 1
CLASSIFICATION:
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TOPOLOGY: 11
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US-08-580-988A-21
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Sequence 3612, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/540,236
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT PILING DATE: 2000-04-04
SEQ ID NOS: 3840
ESCA ID NO 3612
LENGTH: 103
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US-08-464-517-25

Sequence 25. Application US/08464517
; Sequence 25. Application US/08464517
; Patent No. 5869640
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; VORRESPONDENCE ADDRESS:
; ADDRESSE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
                                                                                                                                             Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 4; Length 10
100.0%; Pred. No. 3.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                        Query Match
100.0%; Score 19; DB 2; 1
Best Local Similarity 100.0%; Fred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-007-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                   internal
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US-09-540-236-3612
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CLASSIFICATION: 435
HYPOTHETICAL: no ANT-SENSE; no FRAGMENT TYPE: in ORIGINAL SOURCE: US-08-988-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 VAEF 68
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ZIP: 02109
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APPLICANT: BEACH, David H.
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STREET: MA
COUNTRY: USA
ZIP: 02109
                                                                       100.0%; Score 19; DB 2; Length 106; 100.0%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 19; DB 3; Length 106; 100.0%; Pred. No. 4e+02; tive 0; Mismatches 0; Indels
                                                                                                                        0; Indels
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CLASSIFICATION: 435
FRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
REILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: ISW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 39
1.09-489-039A-8721
1. Sequence 8721, Application US/09489039A
1. Patent No. 6610836
                                                                                                                                                                                                                                                                                                                      US-08-463-772-25; Sequence 25, Application US/08463772; Patent No. 6066501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
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Best Local Similarity 100.
Matches 4; Conservative
                                                                            Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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; MOLECULE TYPE: peptide
US-08-463-772-25
     / MOLECULE TYPE: peptide US-08-246-361A-25
                                                                                                                                                                                                                    66 VAEF 69
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Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 19; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boscon
STATE: MA
COMPUTER: WA
COMPUTER: WA
COMPUTER: READABLE FORM:
MEDIUM TYPE: FOOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION NUMBER: US/08/246,361A
FILING DATE: 16-CCT-1992
FRIOR APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-CCT-1992
FRIOR APPLICATION NUMBER: US 07/963,108
FILING DATE: 16-CCT-1992
PRIOR APPLICATION NUMBER: US 07/868,178
FILING DATE: 16-MAY-1994
APPLICATION NUMBER: US 07/868,178
FILING DATE: 16-MAY-1997
APPLICATION NUMBER: US 07/808,178
FILING DATE: 16-MAY-1997
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAX-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INPORMATION:
TELEPAX: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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REGISTRATION NUMBER: 36,709
REFERNES/DOCKET NUMBER: MII-004C
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 VAEF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VAEF 4
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Sequence 21614, Application US/09252991A

Sequence 21614, Application US/09252991A

Patent No. 655195

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21614
                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 115

LENGTH: 115
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APPLICATIVE GATY PRECON Et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 0.2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h
Similarity 100.0%; Score 19; DB 4; Length 115;
4; Conservative 0; Mismatches 0; Indels
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                                                                                                           Sequence 9915, Application US/09489039A Patent No. 6610836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Klebsiella pneumoniae US-09-489-039A-9915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
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US-09-252-991A-21614
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US-09-489-039A-7200
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GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US 60/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8721
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Sequence 25, Application PC/TUS9305000
GENERAL INFORMATION:
APPLICANT: MINOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 19; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 19; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FPC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIPICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granabar, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECHONICATION INFORMATION:
TELECHONE: 617-861-6240
TELEFAX: 616-861-9540
                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 106 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
WOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 VAEF 46
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66 VAEF 69

us-09-594-978a-2.rai

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138 VAEF 141
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                                                                            JS-09-489-039A-12835
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                                                                                                                                                                                                                                                                                                             Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Swiatlo, Edwin
APPLICANT: Stoke, Walter, Alexis
TITLE OF INVENTION: Pherwococcal Genes, Portions
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIF: 10036
COMPUTER READABLE FORM:
MEDILUM TYPE: Floppy disk
COMPUTER: THE FOODS/MS-DOS
COMPUTER: THE FOODS/MS-DOS
SOFTWARE: PATENTIN FO-DOS/MS-DOS
SOFTWARE: PATENTIN RElease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,055
FILING DATE: 15-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 45-4312-2400
REFERENCE/DOCKET NUMBER: 45-4312-2400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMA
                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 4; I
100.0%; Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
   JMBER: US 60/117,747
1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-529-055-53; Application US/08529055; Patent No. 6592876; GENERAL INFORMATION:
APPLICANT: Briles, David E.
                                                                                                                                                                                                        GRGANISM: Klebsiella pneumoniae US-09-489-039A-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1999-01-7
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7200
LENGTH: 123
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100..
A; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity
Matches 4; Conserv
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COUNTRY:
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Gaps .. 0

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0; Mismatches

4; Conservative

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US-09-1984-52A-167
US-09-1984-52A-167
Sequence 167, Application US/09198452A
Sequence 167, Application US/09198452A
Sequence 167, Application US/09198452A
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment:
TITLE OF INVENTION: Chlamydia pneumoniae genomic for the diagnosis, prev.
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT RILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 167
TYPE: ENGTH: 145
TYPE: PRT
                                                           GENERAL INFORMATION:

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT FELLING NAMER: US 6/117,747

PRIOR APPLICATION NUMBER: US 6/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 143
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Patent No. 647156
RELEATION:
APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al THERAPILICANT: Lynn Doucette-Stamm et al THILD OF INVENTION: WOLLEAGE AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: WORDERC ACID AND AMINO ACID SEQUENCE AND THERAPEUTICS TITLE OF INVENTION: WORDER US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Score 19; DB 4; Length 14
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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100.0%; Pred. No. 5.5e+02;
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Sequence 12835, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Chlamydia pneumoniae US-09-198-452A-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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1100 New York Avenue, N.W., Suite 600
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FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: MCPHAIL, DONALD R.,
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 150 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (202) 371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                   STREET: 1100 mc...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                    COUNTRY: U
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                                                                                                                    100.0%; Score 19; DB 4; Length 145; 100.0%; Pred. No. 5.6e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin RC-Bese #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTONEY AGARM INFORMATION:
NAME: MCCONCATN, WIMBER: 0609.4070002
FELEPRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELEFAK: 202-371-2600
ITELEFAK: 202-371-260
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h Similarity 100.0%; Score 19; DB 2; Similarity 100.0%; Pred. No. 5.8e+02; 4; Conservative 0; Mismatches 0;
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Patent No. 6107514.
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         US-08-460-694-3
; Sequence 3, Application US/08460694
; Patent No. 5858655
; SEQ ID NO 4292
; LENGTH: 145
; TYPE: PRT
; OKGANISM: Enterococcus faecalis
US-09-134-000C-4292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: not relevant
                                                                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                             113 VAEF 116
                                                                                                                                                                                                    1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washi
STATE: DC
COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -08-460-744-3
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/07667711B
; Sequence 3, Application US/07667711B
; Patent No. 6110700
; GENERAL INFORMATION:
TITLE OF INVENTION: Pradl Cyclin and Its CDNA
; TITLE OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
CALF: 2000-
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TAM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-UN-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MCCONATHY, EVelyn H.
REGISTRATION NUMBER: 35,279
REBERENE/DOCKET NUMBER: 0609.4070005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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CORGANISM: Homo sapien
US-09-370-838-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 4, Conserv
           101 VAEF 104
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                                                                                  RESULT 53
US-09-252-991A-20805
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US-09-370-838-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 203
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Sequence 4087, Application US/09134000C
Patent No. 6617156
SERERAL INFORMATION:
APPLICANT: LYAN DOUGETEE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: EMPERACCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4087
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                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 208, Application US/08679493A
Sequence 208, Application US/08679493A
Patent No. 6302295
GENERAL INFORMATION: Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
FILE REPRENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR PILING DATE: 1995-07-14
PRIOR PILING DATE: 1995-07-14
PRIOR FILING DATE: 1995-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 19; DB 4; Length 152; 100.0%; Pred. No. 5.9e+02; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 153;
                                                                                                                                                    Length 150;
                                                                                                                                                                                            0; Indels
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100.0%; Score 19; DB 4; L
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0;
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         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
-07-667-711B-3
LENGTH: 150 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Sest Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 152
TYPE: PRT
ORGANISM: blueshark
                                                                                                                                                                                                                                                                                   66 VAEF 69
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                                                                                                                                                                                                                                                                                                                                                        SULT 51
-08-679-493A-208
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ORGANISM:
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## Sequence 20805, Application US/09252991A
## Sequence 20805, Application US/09252991A
## Patent No. 6521795
## GENERAL INFORMATION:
## SEPLICATION:
## TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
## TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
## TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
## TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
## CURRENT APPLICATION NUMBER: US 60/074,788
## PRIOR FILING DATE: 1999-02-18
## PRIOR FILING DATE: 1998-07-27
## PRIOR FILING DATE: 1998-07-27
## PRIOR FILING DATE: 1998-07-27
## SEQ ID NOS: 33142
## SEQ ID NO 20805
## SEQ ID NOS: 33142
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Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 164;
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100.0%; Pred. No. 6.3e+02;
ive 0; Mismatches 0;
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Patent No. 6444425

Patent No. 6444425

JESTERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Secriet, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIA
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09

EARLIER PLLING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289

SOFTWARE: FastSEQ for Mindows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 55
US-09-540-236-2222
Sequence 2222, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 293274
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                                                              1 VAEF 4
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ ID NO 2222
LENGTH: 166
SEQ ID NO 2222
LENGTH: 166
TYPE: PRT

ORGANISM: M.catarhalis
US-09-540-236-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08471058

Sequence 16, Application US/08471058

Sequence 16, Application US/08471058

GENERAL INFORMATION:
APPLICANT: Kafet.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PREPROF
TITLE OF INVENTION: PREPROF
TITLE OF INVENTION: PREPROF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 19; DB 4; Length 166; Best Local Similarity 100.0%; Pred. No. 6.46+02; Matches 4; Conservative 0; Mismatches 0; Indels
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COMPUTE: CA
COMPUTER READABLE FORM:
MEDIUM TYPE: Disfette
COMPUTER: Disfette
COMPUTER: IBM Compatible
OPERATING SYSTEM: BOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-UN-1995
FILING DATE: 07-COT-1994
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Suban K
REGISTRATION NUMBER: 33,943
REGISTRATION NUMBER: 33,943
REGISTRATION NUMBER: 33,943
TELECOMMUNICATION INFORMATION:
NAME: Lehnhardt, Suban K
REGISTRATION NUMBER: 33,943
FELENCOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415-494-0792
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BESULT 57

US-08-690-095-3

US-08-690-09
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TELEPHONE: 415-855-0555

TELEPAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GERBARK
US-09-113-789-3
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                         1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6034219
GENERAL INFORMATION:
PAPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SECURNCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 1374 Porter Drive
CITY: Palo Alto
STATE: CA
COMPUTER: CA
COMPUTER: EBA Compatible
OOFFATING SYSTEM: DOS
SOFTWARE: FRAESE DISKETE
OOFFATING SYSTEM: DOS
SOFTWARE: FRAESE US/09/113,789
BITTEN NUMBER: US/09/113,789
                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

APPLICATION NUMBER: US/08/471,057

FILING DATE: 07-0CT-1994

ATTORNEY/AGENT INPORMATION:

NAME: LERHHARDT, SUSAN K.

REGISTRATION NUMBER: 33,943

REGISTRATION NUMBER: 33,943

RESERRICE/OFCET NUMBER: 23647-20007.20

TELEPPHONE: (415) 813-5600

TELEPPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0110 US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09113789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 706141
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 1.72 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
         California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 VAEF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VAEF 4
                                 COUNTRY:
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IS-09-113-789-3
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INPORMATION FOR SEA IN NO. 3:

ELENGHH: 172 amino acids

ILENGHH: 172
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Sequence 6739, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: GY09-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6739
LEMORTH 180
TYPE: PRT
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Similarity 100.0%; Pred. No. 7e+02;
4; Conservative 0; Mismatches 0; Indels
                                                                                          Length 174;
                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,980
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08737980;
Patent No. 5843773;
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Apoptosis Regulating Gene
NUMBER OF SEQUENCES: 2
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                       100.0%; Score 19; DB 4; I
100.0%; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 1995-6266
FILING DATE: 24-MRR-1995
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Acinetobacter baumannii
US-09-328-352-6739
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                     Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                77 VAEF 80
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             US-09-489-039A-9869
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US-09-328-352-6739
                                                                                          Query Match
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Patent No. 6610836
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEESIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEESIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEESIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF TILLE OF THE TOWN OF THE TOWN OF THE TOWN AND THE T
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KEVIN G.
PEPTIDE INHIBITORS OF THE P33CDK2 AND
P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN
PAPILLOMAVIRUS E7 ONCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 1; Length 173; 100.0%; Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSER: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZI: 94301
COMPUTER: READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
CURRENT APPLICATION DATA:
RAPLICATION UNMBER: US/08/193,977
FILING DATE: 08-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: ROBINE, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
TYPE: amino acid
                                                                                                                                                                                         Sequence 4, Application US/08193977
Patent No. 5625031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: WEBSTER, KEV
APPLICANT: COLEANN, KEV
TITLE OF INVENTION: P34(
TITLE OF INVENTION: P34(
TITLE OF INVENTION: P34(
CORRESPONDENCES: 34
CORRESPONDENCES: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
SEQ ID NO 9869
LENGTH: 174
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122 VAEF 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Parent No. 6087108

GENERAL INFORMATION:

APPLICANT: Bendern Olga
APPLICANT: Goli, Surya K.

TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 31'4 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTR:.

ZIP: 943.04
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: TOS MINGOWS Version 2.0
                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
FILING DATE: FILED HEREWITH
FILING DATE: FILEWIND DATA:
APPLICATION NUMBER: 36,749
RICHARD DATE: ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1900 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LIBRARY: PROSTUT09
; CLONE: 1646823
US-08-816-241-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 VAEF 107
                                                                           USA
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                                                                                                      ZIP: 94304
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US-09-128-395-1
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                                                                                   Sequence 24341, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24341
LENGTH: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7313, Application US/09543681A
Sequence 7313, Application US/09543681A
Sequence 7315, Application US/09543681A
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7313
LENGTH: 189
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Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0;
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Patent No. 5804185
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Proteus mirabilis -09-543-681A-7313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                .09-252-991A-24341
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EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 85, Application US/09232197A Patent No. 6300096 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 85, Application US/09232201A Patent No. 6348321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Aspergillus nidulans
                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-09-232-200-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                         Best Local Similarity
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Sequence 3800, Application US/09134000C
Sequence 3800, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICATION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR PELING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3800
LENGTH: 194
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100.0%; Pred. No. 7.4e+02;
Live 0; Mismatches 0; Indels
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100.0%; Score 19; DB 4; Length 19
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Sequence 85, Application US/09232200A
Patent No. 6288213
GENERAL INPORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Hordsh, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FAITY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-2193MB
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/093,491
                                                           PF-0239 US
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1646823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecalis
IS-09-134-000C-3800
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 VAEF 118
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IS-09-134-000C-3800
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100.0%; Score 19; DB 3; Length 199; 100.0%; Pred. No. 7.8e+02;
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APPLICANT: Stahl, Andreas
APPLICANT: Lodish, Harvey F.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-2193MC
CURRENT APPLICATION NUMBER: US/09/232,201A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Gladsh, Harvey F.
APPLICANT: Gladsh, Harvey F.
APPLICANT: Gladsh, Harvey F.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REBERRACE: WHI97-2193MA
CURRENT APPLICATION NUMBER: 05/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/031,491
EARLIER APPLICATION NUMBER: 60/033,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASTSEQ for Windows Version 3.0
SERVARE: FASTSEQ for Windows Version 3.0
                                                                      0; Mismatches
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ORIGINAL SOURCE:
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3.09-107-532A-4612
Sequence 4612, Application US/09107532A
Sequence 4612, Application US/09107532A
Sequence 4612, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A DOUCETTE-STAMM ANINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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APPLICANT: Stahl, Andreas.
APPLICANT: Stahl, Andreas.
APPLICANT: Hisch, David J.
APPLICANT: Hisch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ALD TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MD
CURRENT APPLICATION NUMBER: 08/09/232,195A
CURRENT FILLING DATE: 1999-01-04
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER PILLING DATE: 1998-01-05
EARLIER FILLING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILLING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FARESEQ for Windows Version 3.0
SEQ ID NO SES
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 4;
100.0%; Pred. No. 7.8e+02;
tive 0; Mismatches 0;
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER RILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 85, Application US/09232195A
Patent No. 6657049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                      TYPE: PRT
ORGANISM: Aspergillus nidulans
:-09-232-201-85
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4, Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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CONFITER READABLE FORM:

MEDIUM TYPE: CO./ROM ISOSGO

COMBUTING SYSTEM: CIDACHOMIN

OPERATING SYSTEM: CIDACHOMIN

COMBUTING SYSTEM: CIDACHOMIN

APPLICATION NOMBER: US/09/107,532A

APPLICATION NOMBER: US/09/107,532A

APPLICATION NOMBER: US/09/107,532A

APPLICATION NOMBER: 00/085.58

FILLE DESCRIPTION NOMBER: 00/085.58

FILLE OFFICE STORM NOMBER: 00/085.59

APPLICATION NOMBER: 00/085.50

RESULT: TREE CONTRINGEN: 00/085.50

TELECOMPRESSION NOMBER: 00/085.50

COMPRESSION NOMBER: 00/085.50

TITLE OF INVERS ADELIANION NOMBER: 00/085.50

TITLE OF INVERS ADELIANION NOMBER: 00/085.50

TITLE OF INVERS ADELIANION NOMBER: 00/085.50

TITLE OF INVERSION NOMBER: 00/085.50

COMPRESSION NOMBER: 00/085.50

COMPRESSION NOMBER: 00/085.50

TELECOMPRESSION NOMBER: 00/085.70

NATIONS WATCHER: 00/085.70

RESULT NOMBER: 00/085.70

TELECOMPRESSION NOMBER: 00/085.70

TEL
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TELECOMMUNICATION INFORMATION:
TELEPRONE: (212) 278-0400
TELEPAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
TYPE: mino acid
TYPE: problems: fingle
TOPOLOGY: linear
MOLECULE TYPE: protein
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Query Match 100.0%; Score 19; DB 2; Length 205; Best Local Similarity 100.0%; Pred. No. 8e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps <u>≻</u> Ď

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earch completed: May 24, 2004, 17:43:22 ob time : 14 secs

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                                                                                                                                                                        May 24, 2004, 17:34:23 ; Search time 31.7143 Seconds (without alignments) 35.179 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/VEOT_REW_PUB_Pep:*

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18: /cgn2_6/ptodata/1/pubpaa/VEOM_PUB_PEP:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-171-432A-65
US-09-864-761-47201
US-10-424-599-216297
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US-09-791-399-206
US-10-128-711-86
US-10-128-711-145
US-09-908-943A-197
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US-110-39-313A-379
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Sequence 1037, Ap Sequence 1031, Ap Sequence 265337, Sequence 4, Appli Sequence 43750, A Sequence 13355, A Sequence 38, Appli Sequence 227828,	Sequence Sequence Sequence Sequence	Sequence	Sequence	Sequenc	Sequence Sequence	Seguenc	Sequenc Sequenc Sequenc	Sequenc	Sequence	Sequence	ecuences Seguences	Sequenc	Sequenc	Sequenc	Sequenc	Sequenc	Sequenc	Sequenc	Sequenc	Sequence	Sequenc	Sequenc	Seguence	Sequenc	Sequences	Sequence Sequenc Sequenc
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112 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	12 u 12 u 15 u 9 us	122 00 00 00 00 00 00 00 00 00 00 00 00 0	112	277 777 777	12 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	,22	12 13 12 10	12 0	12 14 15 15 15	26 41 25 D	15 14 to 18	12 14	725	121	177	12 14 15 15 15 15 15 15 15 15 15 15 15 15 15	, 12 3 D E	776	212	121	74:	15	5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	191	13 6	1623 1623
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Application US/09791393

Sequence 206, Application No. US20 GENERAL INFORMATION:

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APPLICANT: Herath, Mudiyanselage Athula Chandrasiri,
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri,
APPLICANT: Barekh, Rajesh Bhikhu
APPLICANT: Rohliff, Christian
TITLE OF INVENTION: Proteins, Genes and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: and Unipolar Depression
TITLE OF INVENTION: and Unipolar Depression
TITLE OF INVENTION: and Unipolar Depression
TITLE OF INVENTION and Unipolar Depression
TITLE OF INVENTION NUMBER: US/09/791,393
CURRENT FILING DATE: 2000-02-24
EARLIER PLICATION NUMBER: GB 0034012.3
EARLIER FILING DATE: 2000-12-08
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 308
SECTION 206
                                                                                                                                                                                                             TYPE: PRT;
CRGANISM: homo sapien
US-09-791-393-206
                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-09-791-389-206
US-10-282-122A-54815
US-10-289-762-332
US-10-424-599-25568
US-10-108-260A-4380
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US-10-431-449-6
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2 US-10-380-566-1969

4 US-10-100-957A-142

4 US-10-100-957A-142

4 US-10-100-957A-142

4 US-10-100-957A-142

4 US-10-1088-19

2 US-10-282-122A-65302

US-10-282-122A-65302

US-10-282-122A-65302

US-10-282-122A-65302

US-10-425-114-42248

2 US-10-425-114-42248

2 US-10-425-114-42248

2 US-10-120-801-60

2 US-10-120-801-60

2 US-10-282-123A-58657

US-10-282-123A-58657

US-10-282-123A-58657
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   ESULT 1
S-09-791-378-343
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Gaps

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0; Indels

100.0%; Score 19; DB 10; Length 8; 100.0%; Pred. No. 1e+06;

0, Mismatches

Query Match 100. Best Local Similarity 100. Matches 4; Conservative

1 VAEF

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Sequence 343, Application US/09791378
Sequence 343, Application US/09791378
Parent No. USZOOZO142303A1
Parent No. USZOOZO142303A1
APPLICANT: Parekh, Rajesh
TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: SCHIZOPHRENIA
FILE REFERENCE: 9195-061-999
CURRENT APPLICATION NUMBER: US/09/791.378
CURRENT PILING DATE: 2001-02-23
PRIOR APPLICANION NUMBER: 03/750,395
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SOFTWARE: Patentin Version 3.0
SEQ ID NO 343
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Best Local Similarity 100.
Matches 4; Conservative
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S-09-791-378-343
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Sequence 206, Application US/09791389

Publication No. US2030032773A1

GENERAL INFORMATION:

APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri

APPLICANT: Parekh, Rajesh Bhikhu

APPLICANT: Parekh, Fariesh Bhikhu

APPLICANT: Parekh, Jonathan Alexander

APPLICANT: Terrett, Jonathan Alexander

APPLICANT: Terreth, Jonathan Alexander

APPLICANT: Terrether

APPLICANT: Terr
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ilarity 100.0%; Pred. No. 1e+06;
Conservative 0; Mismatches 0;
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US-09-791-389-206
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                         SETTE, Alessandro D.
CELIS, Esteban
GRAY, Howard
TITLE OF INVENTION: CTL IMMUNITY
CTL IMMUNITY
                                                                                                                                                                                                                                                                                                                                                                 COMPUTE: US

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/128,711

FILING DATE: 22-Apr-2002

CLASSIFICATION: «Unknown»
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                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and C:
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US 07/89,568
FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unianown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 145, Application US/10128711 Publication No. US20030099634A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Parmelee, Steven W.
              Sequence 86, Application US/10128711
Publication No. US20030099634A1
GENERAL INFORMATIONELO, Maria A.
APPLICANT: VITIELO, Maria A.
CHESTNUT, RODERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VITIELLO, Maria A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
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-10-128-711-86
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APPLICANT: Yan, raidang
APPLICANT: Yan, raidang
APPLICANT: Tomasselli, Alfredo G.
APPLICANT: Tomasselli, Mark B.
APPLICANT: Emmons, Mark B.
APPLICANT: Bienkowski, Mike J.
APPLICANT: Bienkowski, Mike J.
APPLICANT: Heinrikson, Robert L.
APPLICANT: PITTE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY FILE REFERENCE: 29915/00201A.US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING CTL INMUNITY
NUMBER OF SEQUENCES: 153
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Batentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,711
RILING DATE: 22-Apr-2002
CLASS:FICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/874,682
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US 07/877,682
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US 07/877,682
FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 14; Length 9; 100.0%; Pred. No. 1e+06; ative 0; Mismatches 0; Indel8
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEO ID NO: 145:
US-10-128-711-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,990
CHESTNUT, Robert W. SETTE, Alessandro D. CELIS, Esteban GRAY, Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT.6
US-09-908-943A-197
I Sequence 197, Application US/09908943A; Publication No. US20030017991A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 623-6793
MATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: Koelsch, Gerald
APPLICANT: Ghosh, Arun K.
TILE GO INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REPERENCE: 2392.1006-007
CURRENT APPLICATION NUMBER: US/10/032,818
CURRENT FILING DATE: 2001-12-28
FRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 14; Length 12; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic peptide US-10-032-818-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 379, Application US/10239313A Publication No. US20030175285A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VARF 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-239-313A-379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-239-313A-379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-119-528-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEATURE: OTHER INFORMATION: Description of artificial sequence: synthetic peptide sequence
                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (4)..(4)
OTHER INVEXTION: amino acid at position 4 has been derivatized with a statine
NAME/KEY: SITE
LOCATION: (10)..(10)
OTHER INFORMATION: amino acid at position 10 has been derivatized with Bodipy FL
IS-09-908-943A-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE

LOCATION: (4)...(4)

OTHER INFORMATION: amino acid at position 4 has been derivatized with a statine
US-08-908-943A-196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 196, Application US/09908943A
Publication No. US20030017991A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GAPPLICANT: Tomasselli, Alfredo G.
APPLICANT: Gurney, Mark B.
APPLICANT: Emmors, Thomas L.
APPLICANT: Benkowski, Mike J.
APPLICANT: Benkowski, Mike J.
APPLICANT: Benkowski, Mike J.
APPLICANT: Highlinkson, Robert L.
APPLICANT: Highlinkson, Robert L.
APPLICANT: Highlinkson, Robert L.
CURRENT FILING DATE: 29918,00281A.USJ.
CURRENT FILING DATE: 2001-07-19
FRICR FILING DATE: 2001-07-19
FRICR FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 19; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 19; DB 12; Length 12; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/908,943A
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,795
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 197
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 197
LENGTH: 10
                                                                                                                                                                                                                TYPE: PRT ORGANISM: synthetic peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/10032818; Publication No. US20330092629A1; GENERAL INFORMATION: APPLICANT: Tang, Jordan J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VAEF 8
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JS-09-908-943A-196
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US-10-032-818-34
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LENGTH: 12
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0; Gaps

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APPLICANT: KLINGUER - HAMOUR, Christine
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORFACH, Liliane
TITLE OF INVENTION: WOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
TITLE OF INVENTION: WOLECULE OF PHARMACEUTICAL OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
CURRENT APPLICATION WUMBER: US/10/239,313A
CURRENT FILING DATE: 2002-09-19
FRIOR APPLICATION NUMBER: PR 00/03711
FRIOR PILING DATE: 2000-03-23
FRIOR PILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 697
SOFTWARE: PETENTIN UNIVER: PROFILE OF SEQ ID NOS: 697
SEQ ID NO 379
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7, Application US/10119528
; Publication No. US20030175722A1
; GENERAL INFORMATION:
; APPLICANT: Mann, M.
; APPLICANT: Mortensen, P.
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING GENOMIC DATABASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 14; Length 13; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
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Length 20;

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NAME/KEY: Peptide LOCATION: 1..20
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                                                                                                                          13 VÀÈF 16
                                                                                 1 VAEF 4
                                                                                                                                                                                        RESULT 12
US-09-171-432A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
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Publication No. US20030187184A1
GENERAL INPRRANTION:
APPLICANT: Fields, Howard A.
APPLICANT: Khudyakov, Yury E.
TITLE OF INVENTION: Antigenically Reactive Regions of the TITLE OF INVENTION: Hepathis A Virus Polyprotein NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALPATIOK SCOCKTON LLP
STREET: 3424 Peachtree Road, N.E.
                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 19; DB 14; Length 15; Best Local Similarity 100.0%; Pred. No. 2e+02; Aatches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
COUNTRY: DSA
COUNTRY: Georgia
COUNTRY: Georgia
COUNTRY: Georgia
ZIP: 30326
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
FILE REFERENCE: MDSP-P01-004
CURRENT APPLICATION NUMBER: US/10/119,528
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/282,51
PRIOR APPLICATION NUMBER: 60/282,51
PRIOR APPLICATION NUMBER: 60/285,362
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 112
SOUTWARE: Patentin Version 3.1
IENGTH: 15
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LOCATION: 1..20
OTHER INFORMATION: /label= XK-1368
3-09-171-432A-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING LAME:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 03063
TELECOMUNICATION INFORMATION:
TELEPHONE: (404) 949-2499
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE GRARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Arabidopsis thaliana
-10-119-528-7
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 VÄEF 13
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FRAGMENT TYPE:
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-09-171-432A-62
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; Sequence 63, Application No. US20030187184A1
; Publication No. US20030187184A1
; GENERAL INFORMATION:
; APPLICANT: Khudyakov, Yury E.
; APPLICANT: Khudyakov, Yury E.
; TITLE OF INVENTION: Hepatitis A Virus Polyprotein
; NUMBER OF SEQUENCES: 8 8
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick Stockton LLP
STREET: 3424 Peachtree Road, N.E.
CITY: Atlanta
STATE: Georgia
; COUNTRY: USA
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                                             Indels
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ZIP: 30326

COMPUTER READABLE FORM:
MEDILUM TYPE: Floppy disk
COMPUTER: IBW PC COMPATIBLE
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIFICATION NUMBER: 03.467
REFERENCE/DOCKET NUMBER: 03.063-0231US
TELEPHONE: (404) 949-2490
TELEPHONE: CARRACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 19; DB 10;
100.0%; Pred. No. 2.6e+02;
iive 0; Mismatches 0;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..20
CTHER INFORMATION: /label= YK-1369
US-09-171-432A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-171-432A-65
Sequence 65, Application US/09171432A
Publication No. US20030187184A1
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
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us-09-594-978a-2.rapb

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and Other Molecules Associated With
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; Sequence 216297, Application US/10424599
; Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Asset TITLE OF INVENTION: Plants and Uses Thereof for Flant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Flant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Flant Improvement
CURRENT FILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 216297
; LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
US-09-864-761-47201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 28;
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
PRIOR PILING DATE: 2001-01-30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 9; I
100.0%; Pred. No. 3.7e+02;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 4; Conserva
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Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Asomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-02-04

PRIOR PRILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 9/632,366

PRIOR FILING DATE: 2000-06-36

PRIOR FILING DATE: 2000-08-36

PRIOR PILING DATE: 2000-08-36

PRIOR FILING DATE: 2000-08-36

PRIOR PILING DATE: 2000-08-36

PRIOR PRILING DATE: 2000-08-36

PRIOR PILING DATE: 2000-08-36
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              APPLICANT: Khudyakov, Yury E.
TITLE OF INVENTION: Antigenically Reactive Regions of the TITLE OF INVENTION: Apparitis A Virus Polyprotein NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick Stockton LLP STREET: 3424 Peachtree Road, N.E.
CITY: Georgia
COUNTRY: Georgia
                                                                                                                                                                                                                                                                                                                                                COUNTRY: USAN
ZIP: 30326
COMPUTER: LOSA
COMPUTER: PIOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE DETAIL RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIFICATION NUMBER: 32,467
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 32,467
TELEPHONE: (404) 949-2400
TELEPHONE: (404) 949-2400
TELEPHONE: (404) 949-2400
TELEPHONE: (404) 949-2400
TELEPHONE: GRAND NO: 65: SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
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OTHER INFORMATION: /label= YK-1832
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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IS-09-864-761-47201
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FILE REFERENCE: 11541-003001
CURRENT APPLICATION NUMBER: US/10/430,752A
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 09/485,286
PRIOR FILING DATE: 2000-02-07
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Best Local Similarity 100...
-... 4; Conservative
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                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-355-570
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Sequence 570, Application US/10242355
Publication No. US20030235331A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENITION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCO03C1
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,897
PRIOR APPLICATION NUMBER: 09/764,897
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/129,065
PRIOR APPLICATION NUMBER: 60/20,14,886
PRIOR FILING DATE: 2000-00-31
PRIOR PELING DATE: 2000-00-629
PRIOR FILING DATE: 2000-00-629
PRIOR PLING DATE: 2000-00-61
PRIOR PILING DATE: 2000-07-11
PRIOR PELING DATE: 2000-07-11
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 100.0%; Score 19; DB 14; Length 35; Similarity 100.0%; Pred. No. 4.7e+02; 4; Conservative 0; Mismatcher
Query Match
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   GENERAL INCOMMENTAL SCHEMENT SCHEMENT: APPLICANT: LOCSMOLE, Sheens M. APPLICANT: LOCSMOLE, Scheme M. APPLICANT: Gentyvers, Anthony B. APPLICANT: Chiryvers, Anthony B. APPLICANT: Charyvers, Anthony B. APPLICANT: Charyvers, Scott APPLICANT: Mixelin, Andrew D. APPLICANT: Mixelin, Anthony H. TILLE OF INVENTION: TRANSFERRIN RECEPTOR GENES FILE REFERENCE: 1038-121 MIS. CURRENT APPLICATION NUMBER: 08/649,518 PRIOR FILING DATE: 1996-05-17 NUMBER OF SEQ ID NOS: 160 SCOFTWARE: PARCHEL PARCHEL PARCHER: PARCHER PARCHER: PARCHER PARCHER: 1996-05-17 SEQ ID NO 69 LENGTH: 35
                                                                                                                                                                                                                                     SULT 16
-10-043-344-69
Sequence 69, Application US/10043344
Publication No. US20030088086A1
GENERAL INFORMATION:
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ORGANISM: Haemophilus influenzae
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Best Local Similarity
Matches 4; Conserv
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PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 570
LENGTH: 37
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Sequence 45, Application US/10430752A

Publication No. US20040005669A1

SERREAL INFORMATION:
APPLICANT: Stahl, Stefan
APPLICANT: Nygen, Per-Ake
APPLICANT: Unlan, Mathias
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF INSULIN
TITLE OF INVENTION: C-PEPTIDE
TITLE OF INVENTION: C-PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 19; DB 15;
100.0%; Pred. No. 4.9e+02;
tive 0; Mismatches 0;
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US-10-424-599-183032
US-10-424
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ORGANISM: Homo sapiens
PRATURE:
OTHER INFORMATION: WAP TO AL035530.11
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.95
OTHER INFORMATION: SWISSPROT HIT: P33485, BVALUE 3.608+00
OTHER INFORMATION: EST_HUMAN HIT: A1765888.1, EVALUE 3.008-18
US-09-864-761-37202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 19; DB 9; Length 43; 100.0%; Pred. No. 5.7e+02;
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-06-30
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Best Local Similarity 100.'
Watches 4; Conservative
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Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharton G.
APPLICANT: Rank, David R.
APPLICANT: Anazel, David K.
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPREBENCE: Aeomica-X.1

CURRENT PILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312
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Publication No. US20030215846A1
GENERAL INFORMATION:
APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: Miverse expression libraries
FILE REFERENCE: FBRIC40.031CP1
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 12000-05-05
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71
LENGTH: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 15; Length 38; 100.0%; Pred. No. 5.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                 PRIOR APPLICATION NUMBER: PCT/GB98/02382
PRIOR FILING DATE: 1998-08-07
PRIOR PILING DATE: 1997-08-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 38
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Lophius piscatorius
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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IS-09-864-761-37202
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S-10-372-003A-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-10-430-752A-45
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Sequence 205632, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 288684
SEQ ID NO 205632
LENGTH: 52
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N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
N: EXPRESSED IN BONE MARROW, SIGNAL = 1
N: EXPRESSED IN HEBLIOO, SIGNAL = 1.1
N: EXPRESSED IN HEBLY, SIGNAL = 1.2
N: EXPRESSED IN HELA: SIGNAL = 1.2
N: EXPRESSED IN HELA: SIGNAL = 1.2
N: EXPRESSED IN PLACENTA, SIGNAL = 2.1
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LENGTH: 48
                            PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN ADULT
OTHER INFORMATION: EXPRESSED IN BETAL
OTHER INFORMATION: EXPRESSED IN BELL
OTHER INFORMATION: EXPRESSED IN HELL
OTHER INFORMATION: EXPRESSED IN HERAL
OTHER INFORMATION: EXPRESSED IN HELA,
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Best Local Similarity
Matches 4; Conserv
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US-10-424-599-205632
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Publication No. US20040031072A1
SENERAL INFORMATION:
BENERAL INFORMATION:
BENERAL INFORMATION:
APPLICANT: La Rosa 1
APPLICANT: Aca Young 3
APPLICANT: Cac Young 4
APPLICANT: Aca Young 5
APPLICANT: Cac Young 5
APPLICANT: Aca Young 6
APPLICANT: Aca Young 7
APPLICANT: Cac Young 7
APPLICANT: Cac Young 7
APPLICANT: Aca Young 7
APPLICANT: Cac Young 7
APPLICANT: Aca Young 7
APPLICANT ACA YOUNG 7
APPLICANT
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Setent No. US20020048763A1
SENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HAnzel, David K.
APPLICANT: HAnzel, David K.
APPLICANT: Gene EXPRESSION ANALYSIS BY MICROARRAY ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILLE OF INVENTION WOMBER: US/09/864,761
CURRENT APPLICATION WOMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-02-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h Similarity 100.0%; Score 19; DB 12; Length 43; Similarity 100.0%; Pred. No. 5.7e+02; 4; Conservative 0; Mismatches 0; Indels
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10-424-599-171318
                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_136291C.1.pep
-10-424-599-183032
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
UNDRER OF SEQ ID NOS: 285684
IENGTH: 43
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                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
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sest Local Similarity
fatches 4; Conserv
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic clone BGF05 with first open reading ; OTHER INFORMATION: frame US-10-372-003A-63
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US-10-372-03A-67

| Sequence 67, Application US/10372003A |
| Publication No. US20030215846A1 |
| GENERAL INFORMATION |
| APPLICANT: Watt, Paul |
| APPLICANT: Thomas, Wayne |
| APPLICANT: Thomas, Wayne |
| APPLICANT: Thomas, Wayne |
| TITLE OF INVENTION: Mathods of constructing and screening |
| TITLE OF INVENTION: Mathods of constructing and screening |
| TITLE OF INVENTION: Mathods of constructing and screening |
| FILE REFRENCE: FERIC40.001CP1 |
| CURRENT APPLICATION NUMBER: US/10/372,003A |
| CURRENT FILING DATE: 2003-02-21 |
| PRIOR APPLICATION NUMBER: US 09/568,229 |
| PRIOR APPLICATION NUMBER: US 60/132,711 |
| PRIOR PILING DATE: 1999-05-05 |
| NUMBER OF SEQ ID NOS: 81 |
| SEX OFFICE OFFIC
                                                                                                                                                                                                                                                                                                                                                                                                                           General Inventoriant
General Inventoriant
General Inventoriant
APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
TITLE OF INVENTION: Methods of constructing and screening
FILE REFRENCE: FBRC40.001CP1
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 69/568,229
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR PLING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63
LENGTH: 55
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100.0%; Score 19; DB 15;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0;
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Pred. No. 7.3e+02;
                                                                                                                                                                                                                               RESULT 28
US-10-372-003A-63
is sequence 63, Application US/10372003A; Publication No. US20030215846A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
PEATURE:
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ORGANISM: Artificial Sequence
FRATURE:
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Best Local Similarity
                                                                                                                 24 VAEF 27
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                                       VAEF 4
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Sequence 233502, Application US/10424599
Sequence 233502, Application US/10424599
Sequence 233502, Application US/10424599
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Sequence 192247, Application US/10424599
Sequence 192247, Application US/20040031072A1
GENERAL INFORMATION:
APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38 = 21(5322) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 192247
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                                                                                                                                                                                                                                                Length 52;
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100.0%; Score 19; DB 12; Length 5
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                OTHER INFORMATION: Clone ID: PAT_MRT3847_27713C.1.pep
S-10-424-599-205632
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S-10-424-599-233502
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OTHER INFORMATION: Clone ID: PAT_MRT3847_1561C.1.pep
S-10-424-1929-192247
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100.0%; Pred, No. 7.3e+02;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                        100.0%; Score 19; DB 12;
100.0%; Pred. No. 6.9e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
TYPE: PRT ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max
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Matches

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US-10-424-599-215734
Sequence 215734, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
Sequence 4, Application US/10219561
Publication No. US20030166567Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               , ORGANISM: Homo sapiens
US-10-219-561-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
Matches 4; Conserv
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US-10-424-599-260762
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JOL210-100 NO. US20030096757A1
SENERAL INFORMATION:
APPLICANT: Weart, Ilona f.
TITLE REFERENCE: 1443.035W01
CURRENT APPLICATION NUMBER: US/10/219,329
CURRENT FILING DATE: 2002-08-15
PRIOR FILING DATE: 2001-08-16
PRIOR PILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Howo sapiens
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100.0%; Score 19; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
     Indels
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     Mismatches
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Best Local Similarity 100.
Matches 4; Conservative
     4; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 VAEF 34
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                                  1 VAEF 4
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10-153-185-4

-10-219-329-4

-10-153-185-4

SULT 32 -10-219-561-4

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(5322)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424
SEQ ID NOS: 285684
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GENERAL INFOGRATION:
APPLICANT: Ouirk, Schehen
APPLICANT: Malik, Schail
APPLICANT: Malik, Schail
APPLICANT: Wilanneva. Julie M.
APPLICANT: Vilanneva. Julie M.
TITLE OF INVENTION: Anti-Acing and Wound Healing Compounds
FILE REFERENCE: 1443.08052
CURRENT APPLICATION NUMBER: US/10/219,561
CURRENT FILING DATE: 2002-08-15
PRIOR FILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
NUMBER: OF SEQ ID NOS: 21
SEQ ID NOS: 21
SEQ ID NOS: 21
LENGTH: 56
LENGTH: 56
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100.0%; Score 19; DB 12; Length 57;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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OCHER INFORMATION: Clone ID: PAT_MRT3847_36836C.1.pep. US-10-424-599-215734
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Publication No. US20040031072A1
GENERAL INPORMATION:
APPLICANT: LA Rosa Thomas J
APPLICANT: Zhou Xihua
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Gaps

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Indels

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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36107C.1.pep
US-10-424-599-214930
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100.0%; Score 19; DB 12;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 214930
LENGTH: 58
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Sequence 214930, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Abou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITIE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
     APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (51223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 57
LENGTH: 57
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S-10-372-003A-75
Sequence 75, Application US/10372003A
Publication No. US20030215846A1
GENERAL INRORMATION:
APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: Methods of CONSTROKT APPLICATION UNMER: US/10/372,003A
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 1999-05-05
PRIOR FILING DATE: 1999-05-05
NUMBER: OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 75
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 15; Length 57; 100.0%; Pred. No. 7.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                      Length 57;
                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                    TYPE: PRT
ORGANIEM: Glycine max
PERATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_77490C.1.pep
S-10-424-599-260762
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100.0%; Score 19; DB 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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Gaps

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APPLICANT: Zuker, Charles S.
APPLICANT: Adder, Uon Elliot
APPLICANT: Adder, Uon Elliot
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Willer, Ken
APPLICANT: The Government of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: T2R, a No. US20040038312Alel Family of Taste Receptors
FILE REFERENCE: 02307E-09802005
CURRENT APPLICATION NUMBER: US/10/364,861
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 95
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Ryba, Nick
APPLICANT: Ryba, Nick
APPLICANT: Mueller, Ken
APPLICANT: Hoon Mark
APPLICANT: Hoon Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Represented by the Secretary of the
APPLICANT: Be represented by the Secretary of the
APPLICANT: Be represented by the Secretary of the
APPLICANT: Bepresented by the Secretary of the
APPLICANT: Bepresented by the Secretary of the
APPLICANT: Bepresented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20030157568Alel Family of Taste Receptors
FILE REPRESENCE: 02307E-098000US
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                                                                                                                                                                                                                                                                                                               Length 68;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 11; 100.0%; Pred. No. 9.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
NUMBER OF SEQ ID NOS: 9068
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/383,982
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Publication No. US20030157568A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 80, Application US/10364861 Publication No. US20040038312A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity luv...
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ORGANISM: Homo sapiens
                                                                                                                                                       TYPE: PRT
CAGANISM: Homo sapiens
US-09-864-408A-40
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LENGTH: 68
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APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVANTON: No. US20040009474Alel Human Polynucleotides and Polypeptides Enco TITLE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR PELLOR OF STATE AND STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Mueller, Ken
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Beresented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20020051997Alel Family of Taste Receptors
FILE REFERENCE: 02307E-098000US
CURRENT PELLING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SEQ ID NO 80
LENGTH: 68
TYPE: POT
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                                                                                                                      FEATURE:
OTHER INFORMATION: MAP TO AC009079.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.54
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BARROW, SIGNAL = 0.65
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48
OTHER INFORMATION: SWISSPROT HIT: P56315, EVALUE 2.00e+00
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100.0%; Score 19; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 19; DB 9; Length 60; Sest Local Similarity 100.0%; Pred. No. 8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: human GR24-09-393-634-80
        LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 VAEF 17
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-09-864-408A-40
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                                                                                                                                     PEATURE:

OTHER INFORMATION: MAP TO AL162171.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71

OTHER INFORMATION: ST HUMAN HIT: BE559987.1, EVALUE 2.00e-03

OTHER INFORMATION: SWISSPROT HIT: P56093, EVALUE 2.00e+00
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 45716 LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 9; I
100.0%; Pred. No. 9.2e+02;
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CONTACTOR:
OURLENGE CARACTORISE POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR FLING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PRECEIT OF SEQ ID NOS: 7059
SOFTWARE: PRECEIT OF SEG ID NOS: 7059
SOFTWARE: PRECEIT OF SEG ID NOS: 7059
SOFTWARE: PRECEIT NOS: 7059
SOFTWARE: PRECEIT NOS: 7059
SOFTWARE: PRECEIT NOS: 7059
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Publication No. US20020197605A1
GENERAL INFORMATION:
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US-09-738-626-5596
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIALI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENCH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100
Matches 4; Conservative
                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 4; Conserv
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Peter No. 1920-2000487531

APPLICANT: Peter, Sharton G.
APPLICANT: Rank, Dariton G.
APPLICANT: Pank, Dariton G.
APPLICANT: Pank, Dariton G.
APPLICANT: Pank, Dariton G.
APPLICANT: Chen, Menahang
TITLE OF INVENTION: HAND GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HAND GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HANDER: US/09/864,761
CURRENY PAPLICATION NUMBER: US/09/864,761
CURRENY PAPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: US/09/862,366
PRIOR APPLICATION NUMBER: US/09/862,366
PRIOR PLINION DATE: 2000-06-32
PRIOR PLINION DATE: 2001-06-30
PRIOR PLINION DATE: 2001-06-30
PRIOR PLINION DATE: 2001-01-30
PRIOR PRIOR PLINION DATE: 2001-01-30
PRIOR PRIOR PLINION DATE: 2001-01-30
PRIOR PRIOR PRIINCHION NUMBER: PCY/USO1/0506
PRIOR PRIINCHION NUMBER: US 09/608/408
PRIOR PRIINCHION NUMBER: US 09/774,203
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                                                                                                                                                                                                                                                                                                                                                               Length 68;
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Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
     CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US/09/393,634
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SEGTWARE: Patentin Ver. 2.1
SEQ ID NO 80
LENGTH: 68
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                               100.0%;
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3-10-383-982-80
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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-09-864-761-45716
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Sequence 30348, Application US/10029386
| Publication No. US20030194704A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G.
| APPLICANT: Rank, David R.
| APPLICANT: Hanzel, David K.
| TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GF TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE PROPERTY FOR GF TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE PROPERTY ACCOUNTS ADDITIONS FILE REFERENCE: AEOMICA-X-2
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5323)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 202605
LENGTH: 71
TYPE: ...
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US-10-424-599-274981

US-10-424-599-274981

US-10-424-599-274981

Sequence 274981, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPREMENCE: 32-21(3223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

NUMBER OP SEQ ID NOS: 285684

SEQ ID NO 274981
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Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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CTHER INFORMATION: Clone ID: PAT_MRT3847_24978C.1.pep.US-10-424-599-202605
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US-10-424-599-274981
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
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Publication No. US20030194704A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HAnzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPRESENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine Vers. 1.1
SEQ ID NO 28645
LENGTH: 70
                                                                                                                                  APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE CO YONGwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 285684
SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 12; Length 69; 100.0%; Pred. No. 9.2e+02; tive 0; Mismatches 0; Indels
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100.0%; Score 19; DB 14; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.6

OTHER INFORMATION: EXPRESSED IN BONE WARROW, SIGNAL = 9.3

OTHER INFORMATION: EXPRESSED IN FLACENTA, SIGNAL = 5.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.7

OTHER INFORMATION: SYRESSED IN HEART, SIGNAL = 9.7

OTHER INFORMATION: SYRESSED IN HEART, SIGNAL = 7

OTHER INFORMATION: SWISSPROT HIT: P78716, EVALUE 3.00e-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT3847_138417C.1.pep
10-424-599-185385
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Publication No. US20040031072A1
GENERAL INFORMATION;
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Best Local Similarity 100..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 VAEF 27
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3-10-424-599-202605
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-10-029-386-28645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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COUNTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: DAN COMPACTION
COMPUTER: TEMPE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: TEMPE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: DAN COMPACTION
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION NUMBER: US/08/894,139
FILING DATE: 13-Aug-1997
ATTORNEY/AGENT TINCANARTION:
NAAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET WUMBER: 32,955
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                               HIJMANS, ELRANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9071, Application US/10156761

Publication No. US2030119018A1

GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISENEA, HARUO
APPLICANT: HEADA UNA
APPLICANT: HORIKAMA, HIROSHI
APPLICANT: HORIKAMA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: APLAYOSHI
APPLICANT: APLAYOSHI
APPLICANT: ALAYOSHI
APPLICANT: ALAYOSHI
APPLICANT: ALAYOSHI
APPLICANT: ALAYOSHI
APPLICANT: ALAYOSHI
APPLICANT: APLATORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9071
LENGTH: 74
TYPE: PRI
                                                                                                                                                 ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLGGY: Linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-214-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 74 amino acids
                                                                                                                                                                                                          CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
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US-10-156-761-9071
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1S-10-029-386-29320
Squence 29320, Application US/10029386
Squence 29320, Application US/10029386
Squence 29320, Application WS. US20030194704A1
GRNERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION HUMBER: US.10/0029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE Annomax Sequence Listing Engine vere: 1.1
SEQ ID NO 29320
LENGTH: 72
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Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO CHR7.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.82

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.73

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1

OTHER INFORMATION: SWISSPROT HIT: P21333, EVALUE 5.00e-22

S-10-029-386-30348
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CTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98

CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99

CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6

CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56

CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.61
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILMG DATE: 2001-12-20
UNUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine ver8, 1.1
ENGIH: 71
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IS-10-214-188-10
IS-10-214-188-10
Sequence 10, Application US/10214188
Publication No. US20030022250A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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0; Gaps

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DOJACTATION TO US20040031072A1
Sequence 253204, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: Excels brink
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Covalic brink
APP
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            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_70669C.1.pep
US-10-424-599-253204
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US-10-424-599-211908
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NAME/KEY: unsure
LOCATION: (1)..(76)
FEATURE INFORMATION: unsure at all Xaa locations
            0; Mismatches
            4, Conservative
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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                                                               1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 55
US-10-424-599-211908
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US-10-424-599-253204
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LENGTH: 77
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            Matches
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CENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38 -21(5322)B

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38 -21(5322)B

CURRENT APPLICANT: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

ELENGTH: 75
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                                                                                 Query Match 100.0%; Score 19; DB 14; Length 74; Sest Local Similarity 100.0%; Pred. No. 9.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Score 19; DB 12; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
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Pred, No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_112004C.1.pep .10-424-599-156128
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THER INFORMATION: Clone ID: PAT_MRT3847_78089C.1.pep
3:10-424-599-261424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (1)..(75)
OTHER INFORMATION: unsure at all Xaa locations
ORGANISM: Streptomyces avermitilis -10.156-761-9071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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Best Local Similarity
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US-10-424-599-162039
US-10-424-599-162039
Sequence 162039, Application US/10424599
Sequence 162039, Application US/10424599
Sequence 162039, Application No. US20040031072A1
Sequence 162039, Application No. US20040031072A1
Septicant: Large Thomas J
APPLICANT: Cao Yongwal
APPLICANT: Cao Yongwal
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 191ants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 162039
LENGTH: 78
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Avalic David K
APPLICANT: Should Related the second Relation of the second Relation Related Related Related Related Related Polymory Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE 39-21 (53.223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
END UN 26.2701
LENGTH: 78
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                                                                                                                                ORGANISM: Homo sapiens
CRGANISM: Homo sapiens
FATURE:
CTHEN INFORMATION: MAP TO ACCOGAIGE.1
OTHEN INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
OTHEN INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHEN INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
OTHEN INFORMATION: SWISSFROT HIT: P14373, EVALUE 7.50e+00
US-10-029-386-32709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Clone ID: PAT_MRT3847_117339C.1.pep US-10-424-599-162039
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARRE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32709
LENGTH: 77
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Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 262701, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 VÀÈF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 VAEF 31
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15-10-029-386-32709
Squence 22709, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
                                                                                                 Sequence 7493, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION:
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: BOSCON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 12; Length 77; 100.0%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Masschusetts
COUNTRY: USA
ZIP: 102109-14875
COMPUTER READBLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Doc-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION DAILS

PRICK APPLICATION NUMBER: 08/993,002

PILING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REPERENCE/DOCKET NUMBER: GIN-018

TELEPANICATION INFORMATION:

TELEPANICATION INFORMATION:

TELEPAN: (617) 742-4214

INFORMATION FOR ENG ID NO: 7499:

SEQUENCE CHARACTERISTICS:

LENGTH: 77 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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LOCATION: (B) LOCATION 1...77
SEQUENCE DESCRIPTION: SEQ ID NO: 7493:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                              8-10-335-977-7493
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RESULT 63
US-09-864-408A-5282
US-09-864-408A-5282
; Sequence 5282, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 125, Application US/10078090; Publication No. US20030044815A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 4; Conservative
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US-10-367-980A-14
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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US-10-078-090-125
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LENGTH: 84
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-10-424-599-216097
Sequence 216097, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Acvalic David K
APPLICANT: Cao Yongwai
APPLICANT: Cao Yongwai
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 99 Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 216097
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                                                                                                                  100.0%; Score 19; DB 12; Length 78; 100.0%; Pred, No. 1e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 80;
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hypeq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
CURENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR FILING DATE: 2000-09-01
NUMBER: OF SEQ ID NOS: 490
LENGTH: 79
                                         FEATURE:
O THER INFORMATION: Clone ID: PAT_MRT3847_79240C.1.pep
10-424-592-262701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
-OTHER INFORMATION: Clone ID: PAT_MRT3847_37165C.1.pep
-07424-599-216097
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100.0%; Score 19; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                      Sequence 368, Application US/10363616 Publication No. US20040044181A1 GENERAL INFORMATION:
                                                                                                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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ORGANISM: Homo sapiens
-10-363-616-368
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ORGANISM: Glycine max
TYPE: PRT
ORGANISM: Glycine max
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-10-363-616-368
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35 VAEF 38

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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Sinkets. Richard A.
APPLICANT: Sinkets. Richard A.
APPLICANT: Sinkets. Richard A.
APPLICANT: Sinkets. Richard A.
CHARANTION: No. U520040009474Alel Human Polynucleotides and Polypeptides Encocryptic of PILE REPERENCE: 21402-012
CURRENT APPLICATION NUMBER: 105/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR APPLICATION NUMBER: 60/206,690
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-367-980A-14

| Sequence 14, Application US/10367980A
| Sequence 14, Application US/10367980A
| Publication No US20030228592A1
| GENERAL INFORMATION:
| APPLICANT: St Vincent's Institute of Medical Research
| APPLICANT: Rogers, Suzanne D
| APPLICANT: Best, James D
| TITLE OF INVENTION: Human Recilitative Glucose Transport Protein GLUT8
| PILE REFERENCE: VS.AJH-IPP17928
| CURRENT FILING DATE: 2003-02-19
| PRIOR PILING DATE: 2003-02-19
| NUMBER OF SEQ ID NOS: 42
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 14
| LENGTH: 82
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Gaps
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100.0%; Score 19; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
PILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_24299C.1.pep
US-10-424-599-201853
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0%; Score 19; DB 12;
Matches 4; Conservative 0; Mismarraria
                                                                                                                                                                                                                                          FEATURE:
NAME/KBY: unsure
LOCATION: (1) .. (85)
UTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-27
PRIOR PILING DATE: 2000-12-27
PRIOR PILING DATE: 2000-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2010-10-216
NUMBER OF SEQ ID NOS: 14110
SOFTWARR: PASESEQ FOR WINDOWS VERSION 4.0
SOFTWARR: PASESEQ FOR WINDOWS VERSION 4.0
                                                 CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 201853
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11224, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Haemophilus influenzae US-09-815-242-11224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen. Kari T.
                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
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APPLICANT: Karra, Ablana APPLICANT: Cafferkey, Robert APPLICANT: Cafferkey, Robert APPLICANT: Cafferkey, Robert APPLICANT: Sun, Yongming APPLICANT: Sun, Yongming APPLICANT: Liu, Chenghua TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and PRILE REPRENCE: DEX.0312
CURRENT APPLICATION NUMBER: US/10/078,090
FRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 210
SOPTWARE: Patentin version 3.1
SEQ ID NO 125
LEMGTH: 84
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Sequence 158536, Application US/10424599
Eublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA Rosa Thomas J
APPLICANT: Expose Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Sol 2013-04-28
NUMBER OF SEQ ID NOS: 285684
EENGTH: 85
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Sequence 20183, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: Anou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT3847_11155C.1.pep S-10-424-599-155636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 19; DB 14; 100.0%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 12;
100.0%; Pred. No. 1.1e+03;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapien
S-10-078-090-125
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1 VAEF 4
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US-10-282-122A-58530
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APPLICANT:
APPLICANT:
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APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Gran, Kari
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: W. H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 2003-02-20
FILE REFERENCE: ELITRA, 2003-02-20
FILE REFERENCE: ELITRA, 2003-02-20
FRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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                                                                                                                             APPLICANT: Haselbeck, Kodert
APPLICANT: Oblean, Kari L.
APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Travick, John D.
APPLICANT: Xu, H Gward
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-3-21
PRIOR APPLICATION NUMBER: G0/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-10-21
PRIOR PLING DATE: 2001-12-2
PRIOR PLING DATE: 2001-12-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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Sequence 11245, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58489, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 4; Conservative
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms;
TITLE REFERENCE: ELITRA.034A
CURRENT PEPPLICATION NUMBER: US/10/282,122A
CURRENT PELLING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/234,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,636
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-27
PRIOR PILING DATE: 2000-10-20-9
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 300-12-16
PRIOR PILING DATE: 300-13-16
PRIOR PILING DATE: 300-13-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 300-10-02-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-282-122A-58489
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Samudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Best Local Similarity 100.
Matches 4; Conservative
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0; Gaps

Indels

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Mismatches

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4; Conservative
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US-10-424-599-180307
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US-10-282-122A-68774
          Matches
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/290, 948
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/200, 335
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2001-02-16
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APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: WITH ROBERT ROB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 76614
SOFTWARE: Patentin version 3.1
LENGTH: 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Haemophilus influenzae
'S-10-282-122A-58530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Pasteurella multocida S-10-282-122A-66960
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Garr, Grant
APPLICANT: Panamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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S-10-282-122A-66960
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PRESENT. 72

19.10-222-1224-6974

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PRESENT. 72

PRESENT. 73

PRESENT. 74

PRESENT. 75

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Search completed: May 24, 2004, 17:42:33 Job time : 32.7143 secs
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SEQ ID NO 245830
LENGTH: 90
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APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 180307
TYPP-
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: A Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38 -21(5322)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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Suguence 360, Application US/10097111
Sublication No. US20030138771A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
THE OF INVENTION: DELLETIER, JERRY
APPLICANT: GROS, PHILLIPPE
APPLICANT: DUBOW, MICHAEL
APPLICANT: DUBOR MAIL-MICROBIAL POLYPEPTIDES
FILE REFERENCE: 073406-0603
FILE REFERENCE: 073406-0603
FILE REFERENCE: 073406-0603
FILE REFERENCE: 000-09-29
PRIOR FILING DATE: 2002-07-24
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 552
SOFTWARE: PACENTIN Ver. 2.1
SEQ ID NO 360
FIRENT: 89
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                                 AAR21549
ABU29329
AAM39361
                                                    ABU46908
AAG91382
AAE30494
                                                                  AAR89212
AAE30503
AAU56508
ABM53027
ABU50525
                                                                                      AAB58972
                                                                                             ABU14941
                                                                                                                            AAM47151 standard; peptide; 6 AA.
12-FEB-2002
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Modular enzyme system; cyclic gene synthesis; repetitive coding sequence; antibiotic; non-ribosomal peptide synthetase; NRPS; PKS; polyketide synthase; actinomycin biosynthase. S chrysomallus actinomycin biosynthase protein acmC fragment #9.

Streptomyces chrysomallus Synthetic.

WO200181564-A2

01-NOV-2001.

25-APR-2001; 2001WO-DE001578.

26-APR-2000; 2000DE-01021267.

(ACTI-) ACTINODRUG PHARM GMBH

Schauwecker F;

2002-049276/06.

N-PSDB; ABA03345

Preparing DNA encoding modular protein for e.g. producing new enzymes for synthesis of polyketide antibiotics, comprises cyclic integration of fragments into a vector.

Example 3; Page 54; 83pp; German.

The present invention relates to the preparation of DNA, in a circular vector, that encodes one or more segments of a modular polypeptide. DNA or DNA libraries produced this way are used to produce modular polypeptides, particularly enzymes, which can be used to act on

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substrates to produce compounds for therapeutic testing. Enzymes of particular interest are those involved in non-ribosomal peptide synthesis or polyketide synthesis, and compounds for testing are particularly macrolide antibiotics, including penicillins, vancomycins or erythromycins, but may also be modular receptors. The present sequence is a fragment of a protein enroded by a Streptomyces chrysomallus actinomycin biosynthesis gene which was used in a plasmid in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. Iike pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
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Tung J, Wang S, Mcconlogue L;
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100.0%; Pred. No. 1.4e+06;
tive 0; Mismatches 0;
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/note= "hydroxyethylene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A beta-secretase inhibitor peptide.
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99US-0139172P.
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sinha S, Tatsuno G,
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15-JUN-1999;
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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of catures containing at least one chosen feature whose relative abundance or predicts the onset or course of VD, especially detecting in a sample of carebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB5S801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or defect of the series of series of series of the series of the series of s
                                                                                                                                                                                                                                                                                                     VD; VD-associated protein isoform; VPI; screening;
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                                                                                                                                                                                                                                                            Vascular dementia-associated protein isoform (VPI) 441.
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                                                                                                                                                                                                                                                                                                                                      diagnosis; prognosis; gene therapy
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                                                                                                        ABB56241 standard; peptide; 8 AA.
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
inhibitor.
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Tung J, Wang S, Mcconlogue L;
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Sequence 7 AA;
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15-JUN-1999;
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Parekh RB, Rohlff C,
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28-DEC-2000; 2000US-00750395.
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
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WO200162785-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8 AA;
                                                                                                                                                                                                 Herath HMAC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                   30-AUG-2001
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AAU26368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest peptides of these proteins. Some of the DPIs (AAU28404-AAU28625) described are decreased in the cerebrospinal fluid (GSF) of BAD (bipolar affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are increased in BAD subjects. Also described are peptide sequences identified from DPI-45 and DPI-213 and the nucleic acid sequence they are encoded by. The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, BP), maniac-depressive illnesses, attention deficit disorders, schizoaffective disorders, and unipolar affective disorders. The present sequence represents one of the DPI tryptic digest peptides of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-218; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
                                                  Human, depression associated protein isoform, tryptic digest peptide, DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder; neuropsychiatric disorder; bipolar mood disorder; neuroleptic; maniac-depressive illness; schizoaffective disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                      Terrett JA, Tyson KL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 4; Le 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                     (OXFO-) OXFORD GLYCOSCIENCES UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                    Herath HMAC, Parekh RB, Rohlff C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 37; 153pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU25114 standard; peptide; 8 AA.
                   DPI tryptic digest peptide #317.
                                                                                                                                                                                                                                                                                           24-FEB-2000; 2000GB-0004412.
08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
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les 4; Conserv
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Matches 4
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RESULT 6 AAU251

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New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents a schizophrenia-associated protein isoform (SPI)
These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
in cerebrospinal fluid, serum or plasma and are useful markers of
schizophrenia. The sequences can be used for treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, Bipolar Affective Disorder, BAD, Depression-Associated feature, DF, Depression-Associated protein isoform, DF; Cerebro-epinal fluid, CSF, antidepressant; antimanic, nootropic, tranquiliser, neuroleptic, attention deflicient disorder; schizoaffective disorder;
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Tyson
Terrett JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Depression-Associated Protein isoform DPI-124.
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WPI; 2001-582081/65

AAU15458 standard; peptide; 8 AA 23-FEB-2001; 2001WO-GB000783 Herath HMAC, Parekh RB, 24-0CT-2001 ESULT 8 AU15458

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Preparation for diagnosing or treating bipolar affected disorder (BAD) or unipolar depression, or for screening for modulators, comprises a BAD-associated protein isoform.
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Claim 8; Page 37; 163pp; English

The invention relates to a preparation comprising an isolated Bipolar Affected Disorder (BAD)-Associated Protein Isoform (DPIS). The DPI's are used to screen, diagnose or prognose of BAD or unipolar depression, identify a chermine the stage or severity of BAD or unipolar depression, identify a subject at risk of developing BAD or unipolar depression, or monitor the effect of therapy in a subject. They are also used to screen for or identify agents that interact with a DPI. These agents, antibodies against the DPIs, and nucleic acids encoding the DPIs are used to treat or prevent BAD or unipolar depression. Diseases that can be treated are attention deficient disorder. The DPIs are used in proteomics. The unipolar affective disorder. The DPIs are used in proteomics. The DPIs are used in proteomics. The bollons of using DPIs for screening, diagnosis of BAD or unipolar depression overcomes the problems of using gene expression analysis, such as not being able to obtain central nervous present sequence is a DIP increased in the CSF (cerebro-spinal fluid) of subjects having BAD

Sequence 8 AA;

ö Gaps ô 0; Indels 95.0%; Score 19; DB 4; Length 8; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels 4; Conservative Local Similarity Query Match Best Loc Matches

2 VAEF 5

2 VARF 5

AAU15458;

Schizophrenia-associated isoform peptide #343.

Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder; neurological disorder; neuropathy.

Homo sapiens

WO200163293-A2.

30-AUG-2001.

24-FEB-2000; 2000GB-0000415. 28-DEC-2000; 2000US-00750395.

(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

Rohlff C;

WPI; 2001-502868/55.

Diagnosing and monitoring Schlzophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.

Claim 6; Page 36; 160pp; English

The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH. Associated Protein Insoforms (SPIS) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential charapeutic agents. The method is used for (1) screening or diagnosis of SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH and (2) monitoring the effect of therapy adminiscered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFs, SPIS and related molecules (e.g. secondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment and as targets to secondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment of the progress of the disorders such as SCH from neurological disorders, where neuropsychiatric disorders such as SCH from neurological disorders, where manifestations of antomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular canaative defects and neuropsychiatric disorders. Adults and encusopsychiatric disorders and the invention cellular and of the invention

Sequence 8 AA;

ö Gaps ö 0; Indels 95.0%; Score 19; DB 4; Le 100.0%; Pred. No. 1.4e+06; iive 0; Mismatches 0; 4; Conservative Query Match Best Local Similarity Matches 4; Conserva

2 VAEF 5

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AAR78909 standard; peptide; 9 AA.

(first entry) (revised) 25-MAR-2003 27-MAR-1996 AAR78909;

MAGE 3 105-113 cytotoxic T lymphocyte epitope.

MAGE 3 105-113; cytotoxic T; CTL; epitope; helper T; HTL; cell; lymphocyte; antigens; treatment; disease prevention; tumours; cancer;

Homo sapiens.

WO9522317-A1

95WO-US002121. 94US-00197484. 16-FEB-1994; 16-FEB-1995; 

(CYTE-) CYTEL

ï Celis E, Sette AD, Chesnut RW, Vitiello MA,

WPI; 1995-302545/39.

and B. Compsn. inducing cytotoxic T lymphocyte response to pref. viral, bacterial, parasitic or tumour antigens - useful in the treatment prevention of diseases associated with the antigen e.g. hepatitis

Example 13; Page 71; 109pp; English

A compsn. which induces a cytotoxic T lymphocyte (CTL) response

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Gaps

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Db 5, 1.4e+06; - 0, Indels

Length 9;

DB 5;

95.0%; Score 19; DB 100.0%; Pred. No. 1.4 iive 0; Mismatches

llarity 100.0%; P: Conservative 0;

Best Local Similarity
Matches 4; Conser

Query Match

w 6 VAEF 9

2 VAEF

ਨੇ g Beta-secretase, enzyme; cleavage site; amyloid protein precursor; APP; aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;

aspartyl protease; n Alzheimer's disease.

sapiens

Synthetic.

Beta-secretase related peptide SEQ ID NO:197.

(first entry)

31-MAY-2002

ABB06593;

ABB06593 standard; peptide; 10 AA.

RESULT 11

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The present sequence represents a beta-amyloid precursor protein (APP) inhibitor peptide. This peptide inhibits binding between APP and BACE (beta site APP cleaving enzyme). The specification describes a crystallized complex of BACE and the present APP inhibitor. Protein coordinate data for BACE is given in the specification. The APP inhibitor peptide is based on the P10 to P4' APPPSI Swedish family mutation. The crystallized complex is used for identifying an agent that interacts with an active site of BACE or an active site of an APP binding protein or peptide. The agents are useful in the treatment and/or prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crystallized complex of beta-gite amyloid precursor protein (APP) cleaving enzyme (BACB) and APP inhibitor peptide useful for identifying agents that interact with active site of BACB or active site of APP binding protein or peptide.
human MAGE antigen (Ag) in a mammal comprises, a MAGE CTL Ag response inducing peptide (i.e. AAR789104 to AAR78917) and a lipid conjugated helper T cell inducing peptide. The compsn. is useful in the treatment and prevention of MAGE tumour Ag associated diseases, e.g. melanoma cancers. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-amyloid precursor protein, APP, APP inhibitor peptide, BACE, beta site APP cleaving enzyme; protein coordinate data, APP751; Swedish family mutation, Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stahl ML;
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                                                                                                                                                                                                                                                                                                                                                                                                                               A beta-amyloid precursor protein (APP) inhibitor peptide.
                                                                                                                                      Query Match 95.0%; Score 19; DB 2; Length 9; Best Local Similarity 100.0%; Pred, No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                           ABB77871 standard; peptide; 9 AA
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/note= "statine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Svenson K, Annis B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-2000; 2000US-0234576P.
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Misc-difference
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                                                                                                       Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
Homo sapiens.
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Somers WS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
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Alzheimer's disease

Sequence 9 AA;

Novel substrates for human aspartyl protease useful for identifying modulators of beta secretase activity of aspartyl protease for treating

Bienkowski MJ;

Emmons TL,

Gurney ME,

Tomasselli AG,

Heinrikson RL;

Yan R,

WPI; 2002-216995/27.

Alzheimer's disease.

(PHAA ) PHARMACIA & UPJOHN CO

19-JUL-2001; 2001WO-US023035. 19-JUL-2000; 2000US-0219795P. 12-MAR-2001; 2001US-0275251P.

WO200206306-A2.

24-JAN-2002

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(first entry)
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                                                                                                                                                                                            WO200253594-A2.
                                                                                                                                            sapiens.
15-NOV-2002
                                                                                                                                                                                                                            11-JUL-2002
                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                  Tang JJN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated peptide (I) comprising a sequence of at least four amino acids, where the peptide is a substrate for conducting aspartyl protease assays. (I) has neuroprotective and notropic activities, and can be used as an inhibitor of beta-secretase activity. A beta-secretase modulator from the present invention can be used for inhibiting beta-secretase activity in vivo, and in the manufacture of a medicament for the treatment of Alzheimer's disease. Pharmaceutical compositions from the present invention can be used for treating a disease or condition characterised by an abnormal beta-secretase activity. (I) is useful for identifying agents that modulate the activity of human hap2 aspartyl protease (Hu-Asp3). (I) is useful as a core structure to construct derivatives. ABL49914 to ABL49925 and ABB06409 to ABB06593 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                          Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP; aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel substrates for human aspartyl protease useful for identifying modulators of beta secretase activity of aspartyl protease for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bienkowski MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 5; Length 12; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Emmons TL,
                                                                                                                                                               Beta-secretase related peptide SEQ ID NO:196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 188; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tomasselli AG, Gurney ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG78404 standard; peptide; 12 AA.
                                                                   ABB06592 standard; peptide; 12 AA
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12-MAR-2001; 2001US-0275251P.
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                                                                                                                                (first entry)
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-216995/27.
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                                                                                                                                                                                                                                                                                                           WO200206306-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heinrikson RL;
                                                                                                                                31-MAY-2002
                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                          24-JAN-2002
                                                                                                                                                                                                                                                               Homo sapie
Synthetic.
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ABG78404;

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The invention relates to an inhibitor of catalytically active memapsin 2 (an aspartic protease which can cleave at beta secretase sites), which binds to the active site of memapsin 2 defined by the presence of two catalytic aspartic residues and substrate binding cleft. Also included is a method of determination of the substrate side-chain preference in memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2 substrates; (a) reacting a mixture of memapsin 2 substrates; or (b) prespring a combinatorial intrary of memapsin 2 substrates; or (b) prespring a combinatorial intrary of memapsin 2 inhibitors containing a base sequence taken from ownsy-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 inhibitors containing a base sequence taken from ownsy-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 and detecting the bound memapsin 2 with an artibody raised to memapsin 2 and an alkaline phosphatase conjugated secondary antibody. The inhibitors may be used in the manufacture of a medicament for the treatment of Alaheimer's disease since memapsin 2 may be involved in the cleavage of amyloid precursor protein (APP), and for determining the substrate side-chain preference in memapsin 2 sub-sites.

The present sequence represents a subsite variant peptide used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
                                                                  Human; memapsin 2; aspartic protease; beta secretase; degenerative disease; Alzheimer's disease; amyloid precursor protein; APP; neuroprotective; nootropic; inhibitor; substrate side-chain preference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Memapsin 2 substrate specificity determination peptide #10.
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OKLA-) OKLAHOMA MEDICAL RES FOUND. (UNII ) UNIV ILLINOIS FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 51; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ghosh AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-2001; 2001WO-US050826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2000; 2000US-0258705P.
14-MAR-2001; 2001US-0275756P.
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ADD35467
ID ADD35.
XX
AC ADD35.
XX
DT 15-JAN
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22-MAR-2001; 2001WO-FR000872.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VARF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13 AA;
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                                                            WO200047618-A2
                                                                                                                                                     10-FEB-1999;
15-JUN-1999;
                                                                                                                                                                                                                                    Anderson JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-2001
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                                                                                            17-AUG-2000
inhibitor.
                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM99276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises a crystallised recombinant protein that is involved in general metabolism, the recombinant protein may be from staphylococcus aureus, Streptococcus puneunniae, Helicobacter pylori, Escherichia coli or Pesudomonas aeruginosa. The crystallised recombinant protein of the invention is useful in the prevention (vaccine) or treatment of a disease or disorder caused by S. pneumoniae, H. pylori, S. coli or P. aeruginosa. The present amino acid sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Vedadi M, Alam MZ, Awrey D, Beattie B;
, Houston S, Mansoury K, Necakov S, Nethery K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae, Helicobacter pylori or Pseudomonas aeruginosa involved in general metabolism, useful as drug targets for pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
                              crystallised recombinant protein; metabolism; Staphylococcus aureus; Streptococcus pneumoniae; Helicobacter pylori; Escherichia coli; Pseudomonas aeruginosa; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gabs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mansoury K, Ne F, Wrezel O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           on S, Mansc
Vallee F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, SEQ ID NO 66; 277pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A beta-secretase inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Edwards A, Dharamsi A, Vedadi M,
Canadien V, Domagala M, Houston
Ng I, Pinder B, Sheldrick B, Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB07889 standard; peptide; 13 AA.
 Escherichia coli DnaK peptide #3
                                                                                                                                                                                                                 21-NOV-2001; 2001US-0332160P.
27-NOV-2001; 2001US-0333661P.
27-NOV-2001; 2001US-0333661P.
18-DEC-2001; 2001US-0341770P.
19-DEC-2001; 2001US-0341954P.
19-DEC-2001; 2001US-0342542P.
20-DEC-2001; 2001US-03442582P.
28-DEC-2001; 2001US-03445582P.
28-DEC-2001; 2001US-0343506P.
                                                                                                                                                                                        21-NOV-2002; 2002WO-CA001768
                                                                                                                                                                                                                                                                                                                                                                                 28-DEC-2001; 2001US-0343679P.
                                                                                                                                                                                                                                                                                                                                                                                                               (AFFI-) AFFINIUM PHARM INC.
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Best Local Similarity
Matches 4; Conserv
                                                                                            Escherichia coli.
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                                                                                                                            WO2003044185-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Edwards A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-2000
                                                                                                                                                        30-MAY-2003
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AAB07889
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Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC; immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal; bactericidal; antiparasitic; fungicidal; cytostatic; medicine; pharmaceutical; immune deficiency; autoimmune; hypersensitivity; allergy; graft rejection; infection; hormonal disorder; central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid petide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzhaimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzhaimer's disease or Alzhaimer's disease. Itke pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzhaimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification describes a beta-secretase enzyme. The enzyme cleaves
                                                                                                                                                                                                                                                                                                                                                                                                                                         Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
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                                                                                                                                                                                                                                                        Power M;
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                                                                                                                                                                                                                                                    Doane MT, Frigon N, John V,
Tung J, Wang S, Mcconlogue L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 33; Page 24; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM99276 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                 Tung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity 100.0%;
4; Conservative 0
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human immunodeficiency virus
10-FEB-2000; 2000WO-US003819.
                                                                    99US-0119571P.
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                                                                                                                                                                                    (ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                Basi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                 Tatsuno G,
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-533011/48.
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Tue May 25 09:26:06 2004

us-09-594-978a-3.rag

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10-FEB-1999;
15-JUN-1999;
                                                                                Homo sapiens
                                                                     14-NOV-2000
                                                                                     17-AUG-2000
                                                                   AAB07888;
                                                             RESULT 17
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Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; eurorpordective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoletin, apoptosis related protein; cadherin; cyclih; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interleukin; G-protein coupled receptor; thiosesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-like pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
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                                                                                                                                                                                                                                                                    rurified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represents a peptide derived from beta-amyloid precursor protein
                                                                                          Power M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 3; Length 14; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
                                                                                          Frigon N, John V,
ng S, Mcconlogue L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human peptide #735 encoded by a SNP oligonucleotide.
                                                                                          Doane MT, Frigo
Tung J, Wang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 12; 121pp; English.
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27-DEC-2000; 2000US-00173419.
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(ELAN-) ELAN PHARM INC
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                                                                                          Basi G,
                                                                                     Anderson JP, Basi G,
Sinha S, Tatsuno G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 VAEF 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a pharmaceutical compound (I) that contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in the form of an addition salt with a strong, physiologically acceptable acid (II). Also described are: (a) a pharmaceutical composition acid (II). Also described are: (b) a pharmaceutical composition containing at least one (I); (b) a vaccine containing at least one (I); (c) a method for in vitro diagnosis of diseases associated with the presence of (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process for preparing (I). (I) has immunomediater, endocrine, antiallergic, oneuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and cytostatic activities. (I) are useful, in human or veterinary medicine, in pharmaceutical compositions (for treating immune disorders, e.g. in pharmaceutical compositions (for treating immune disorders, e.g. in pharmaceutical compositions (for treating immune disorders efor residention, infection, hormonal disorders and central nervous system cisection, infection, hormonal disorders and central nervous system creatment or prevention of: (i) viral, bacterial, parasitic or fungal infections, or (ii) of cancers. A particular application is in antimelanoma vaccines. (I) are also useful for in vitro diagnosis of diseases associated with interactions between MHC and (I), e.g. melanoma and human immunodeficiency vitus infection. AAM98988 to AAM95922 represent invention immune immunodeficiency vitus infection compounds from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                 Stabilized pharmaceutical containing N-terminal glutamic acid or glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt with strong acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 4; Length 13; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                      Goetsch L;
                                                                                                                                                                                                                                      Corvaia N, Beck A,
                                                                                                                                       (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                  23-MAR-2000; 2000FR-00003711
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Best Local Similarity الاست.
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The present invention relates to oligomuclectides (see AAL26793-AAL34659)
encoding polymorphic variants of proteins related to amylases, amyloid
proteins, anglopoletin, apoptosis related proteins, cadherin, cyclin,
polymerase, oncogenes, histones, kinases, colony stimulating factors,
complement related proteins, cytochromes, kinesins, cytokines,
interferons, interleukins, G-protein coupled receptors and thioesterases.
The present sequence is a peptide encoded by one such oligomucleotide.
The oligomucleotides and the peptides encoded by them may be used in the
prevention, diagnosis and treatment of diseases associated with
prevented, diagnosed and/or treated include multifactorial diseases
with a genetic component, such as autoimmune diseases (e.g. rheumatoid
arthritis, multiple solerosis, diabetes, systemic lupus erythromatosus
and Grave's disease), inflammation, cancer (e.g. cancers of the nervous
brain, breast, colon and kidney, leukemial), diseases of the nervous
system and an infection of pathogenic organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic database; mass spectrometer; proteomic business; pharmaceutical; nuclear transport; signalling pathway; cellular organelle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying coding sequence in genomic databases for conducting protecomics business, by using polypeptide sequence information obtained from peptide sequencing projects, especially those using mass spectrometers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 4; Length 14; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
                                       Disclosure; Page 3829; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana S11 peptide #6.
autoimmune diseases and infections.
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20-APR-2001; 2001US-0285362P.
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Best Local Similarity
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also used for establishing a distribution system for distributing the pharmacutical preparation for sale, and may optionally include establishing a sales group for marketing the pharmacutical preparation. It is also used for predicting the gene structure, such as intron/exon boundaries; for searching genomic datebases for sequences derived from multi-protein complexes e.g. assemblies with a particular function such as splicing, transport or nuclear import or export; for elucidating transfer than structural complexes (that are involved in signalling pathways) and for identifiang proteins in cellular organales. The present sequence is Arabidopsis thaliana peptide used to illustrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides AAW42943-46 are immunogenic peptides corresponding to immunogenic epitopes of the Hepatitis A virus (HAV). The peptides are ubstantially shinlar to a portion of the amino acid sequence of the P3A protein of HAV corresponding to amino acids 1433-1496. The present peptide is derived from amino acids 1430-1449 and has a reactivity of 58.5% with acute sera. Compositions containing the peptides can be used to induce an immune response to HAV in a mammal. The peptides can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptides can also be used to make an antibody against HAV by
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                                                                                                                                                                                                                                                95.0%; Score 19; DB 6; Length 15; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic Hepatitis A virus peptide YK-1369.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW42944 standard; peptide; 20 AA.
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                                                                                                                                                                                the method of the invention
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                                                                                                                                                                                                                                                                 Local Similarity
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13 VAEF 16
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Matches
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                                                                                                                                                                                                                                  Immunogenic peptide; immunogenic epitope; P3A protein; immune response;
             Gaps
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 100.0%; Pred. No. 2.6e+02;
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0;
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(D AAB69462 standard; peptide; 21 AA.
CX (X AAB69462;
(C AAB69462;
Y 20-APR-2001 (first entry)
                                                                                                                            AAW42943 standard; peptide; 20 AA.
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            4; Conservative
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  Best Local Similarity
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The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comparise antigenic epitopes of the major structural capsid polypeptides or non-structural polypeptides of HAV with one or more glutamine or non-structural polypeptides of HAV with one or more glutamine concerns at the carboxy end of the peptide. The peptides are used to detect the presence of Antibodies against HAV in mammalian serum, to detect the presence of HAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting ISM antibodies in mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or lelectrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end the peptides enhances the ISM antibody reactivity
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                                                                               Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
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Synthetic HAV P3A peptide, SEQ ID NO: 62.
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Synthetic.
                                                                                                                                                                                                                      Hepatitis A virus
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WPI; 1997-535831/49.

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The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise anigenic epitopes of the major structural capsid polypeptides or non-structural polypeptides of the peptide. The peptides are used to detect the presence of HAV in a human or animal through the binding of the peptide to an antibodies against HAV in mammalian serum, to detect the presence of HAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting Ism antibodies in mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a mammalian serum and adtecting of samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutanine at the carboxy end of the peptides enhances the IgM antibody reactivity
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                                                                                             14-JUL-2000; 2000WO-US019267
                                                                                                                                                                  99US-0144412P
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                                                                                                                                                                                                                                                                                                   Khudyakov YE;
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                                25-JAN-2001.
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AAW42946
EXEXEXEXEX SON X EXEXEX EXEXEX EXEXEX EXEXEX EXEXEX EXEXEX EXEX EX
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                                                                                                                                         The present immunogenic peptide corresponds to an immunogenic epitope of the Hepatitis A virus (HAV). The peptide is substantially similar to a portion of the amino acid sequence of the PJA protein of HAV corresponding to amino acids 1423-1496. Compositions containing the peptide can be used to induce an immune response to HAV in a mammal. The peptide can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptide can also be used to make an antibody against HAV by administering the peptide to a mammal
                                        Immunogenic Hepatitis A Virus (HAV) peptide(8) - used to induce an immune response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprises antispenic epitopes of the major structural capsid polypeptides or non-structural polypeptides of HAV with one or more glutamine molecules at the carboxy end of the peptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to the peptide to an antibody, to detect acute phase infection by detecting ISM antibodies in mammalian serum and detecting convalescence in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                             Length 25;
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                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 100.0%; Pred. No. 3.3
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                                                                                                               Claim 33; Page 115; 140pp; English.
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Best Local Similarity 100...
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                3 VAEF 6
                                                                                                                                                                                                                                                                                               Sequence 25 AA;
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Peptide #7947 encoded by probe for measuring placental gene expression

(first entry)

17-0CT-2001

AAM33910;

AAM33910 standard; protein; 28 AA.

Probe; microarray; human; placenta; antenatal diagnosis;

genetic disorder

WO200157272-A2

09-AUG-2001

Homo sapiens.

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Gaps

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mammal. The peptides are used to detect or quantify HAV antibodies in samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, rareking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the IgM antibody reactivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human mevalonate pyrophosphate decarboxylase coding sequence - used for screening for MPD inhibitors, which regulate and control cholesterol
                                                                                                                                                                                                                                                                                                                                                                        Human mevalonate pyrophosphate decarboxylase peptide NT71.
                                                                                                                                        95.0%; Score 19; DB 4; Length 25; 100.0%; Pred. No. 3.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Mevalonate pyrophosphate decarboxylase; MPD; cholesterol.
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                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                   4; Conservative
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                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                                                                                         3 VAEF 6
                                                                                                                 Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09714787-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-1995;
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Matches
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Peptide NT71 (AAW17832) was obtd. by trypsin digestion of human liver mevalonate pyrophosphate decarboxylase (MPD) (AAW17831), an enzyme of the cholesterol biosynthetic pathway. The sequence of the peptide was used to design PCR primers utilised in the amplification of cDMA from a rat liver cDNA library. A rat MPD partial clone was obtd. and used as a probe to screen a human liver cDNA library. A 1800 bp sequence (AAT66464) coding for human MPD was identified

Sequence 28 AA;

ö Gaps ö 95.0%; Score 19; DB 2; Length 28; 100.0%; Pred. No. 3.7e+02; ive 0; Mismatches 0; Indels 4; Conservative Query Match Best Local Similarity Matches 4; Conserv

23 VAEF 20

RESULT 27

2 VAEF 5

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Gaps
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hypercholesterolaemia; coronary heart disease.
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Similarity 100.0%; Score 19; DB 4; Length 28;
4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      Human liver peptide, SEQ ID No 34112.
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                                                                                                                        ABG55464 standard; peptide; 28
                                                                                                                                                                    (first
    Query Match
Best Local Similarity
Matches 4; Conserv
                                               2 VAEF 5
                                                                   4 VAEF 7
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                                                                                                                                                                                                                                              Homo sapiens.
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.

Chen W, Rank DR;

Hanzel DK,

Penn SG,

WPI; 2001-488897/53

(MOLE-) MOLECULAR DYNAMICS INC

21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.

04-FEB-2000; 2000US-0180312P. 26-MAY-2000; 2000US-0207456P. 30-UUN-2000; 2000US-00608408. 03-AUG-2000; 2000US-00632366.

30-JAN-2001; 2001WO-US000663.

Claim 27; SEQ ID NO 34179; 654pp; English.

The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal disgnosis of

human genetic disorders

Sequence 28 AA;

2000US-0180312P

Chen W, Rank DR;

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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 11109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. Assorbables here single exon encoded peptides of the invention. Note: The sequence lifermation for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
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                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 34112; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG43601 standard; peptide; 28 AA.
                                                                                                      26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-02608408.
03-AUG-2000; 2000US-00632566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                     30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                         Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                              WPI; 2001-488898/53
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28 AA;
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                                                                                          04-FEB-2000;
                 09-AUG-2001
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ABG43601
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0; Gaps

Length 28; 0; Indels

95.0%; Score 19; DB 4; Le 100.0%; Pred. No. 3.7e+02; tive 0; Mismatches 0;

(first entry)

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Complements or the 1287 open reading frames derived from the 12614

complements or the 1287 open reading frames derived from the 12614

complements or the 1287 open reading frames derived from the 12614

complements of probes which hybridise at high stringency to a mucleic

control for the novel set of probes which hybridise at high stringency to a mucleic

control set of probes which hybridise at high stringency to a mucleic

control from human lung, comprising (a) contracting the array with a sample

collection of detectably labeled nucleic acids derived from human lung

collection of detectably labeled nucleic acids derived from human lung

collection of detectably bound to each probe of the extray; identifying exons in a eukaryotic genome, comprising (a)

algorithmically predicting at least one exon from genomic sequences of

the enkaryote; and (b) detecting appecific hybridisation of detectably

collection and the expression of each of the method

comprising (a) identifying exons from genomic sequence by the method

comprising (a) identifying exons from genomic sequence by the method

comprising (a) identifying exons from genomic sequence by the method

comprising (a) identifying exons from genomic sequence by the method

comprising (a) identifying exons from genomic sequence by the method

comprising (b) measuring the expression of each of the exons in several

control to a sequence with the exon, where a common pattern of

control to a sequence, mentioned in the specification, or encoded by the

conter, chronic obstructive pulmonary disease such as asthma, lung

cancer, chronic obstructive pulmonary disease such as asthma, und

conter, chronic obstructive pulmonary disease (COPD), interstitial lung

cancer, chronic obstructive pulmonary disease (COPD), interstitial lung

cancer, chronic obstructive pulmonary disease such as asthman shouls solerosis, gaucher's glasses, Niemann-Pick disease, Hermansky-

chiscages and for the erype pulmonary disease, pulmorary alveolar proteinosis, pulmonary hypensents sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their
                                                                                                                                                                                                                                                                                                                                                                                                      Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 33266; 634pp; English
                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR,
                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                         2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
                                                          30-JAN-2001; 2001WO-US000665.
                                                                                                                           2000US-0207456F.
2000US-00608408.
                                                                                                                                                                         2000US-00632366
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                                                                                                                                                                                                                                                                                                                         Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-114183/15
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Best Local Similarity
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                    15-NOV-2001
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2000US-0233064P.
2000US-0233065P.
2000US-0234223P.
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2000US-0229343P.
2000US-0229344P.
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22-AUG-2000; 2000US-0226681F.
22-AUG-2000; 2000US-0226868F.
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2000US-0231413P.
2000US-0231414P.
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14-AUG-2000; 2000US-0225758P.
14-AUG-2000; 2000US-0225759P.
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23-AUG-2000; 2000US-0227009P.
30-AUG-2000; 2000US-0228924P.
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000US-0229513P.
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                             17-JAN-2001; 2001WO-US001354
09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a Streptococcal polypeptide. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
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                                                                                                                                                                    Polypeptide, ORF, open reading frame; infection; bacterial; streptococcal; bacteremia; diagnosis; prophylaxis.
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Reid RH, Zarfos PN;
                                                                                                                                          Streptococcus pneumoniae polypeptide.
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                                               AAW62760 standard; protein; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 32; 181pp; English
                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                             (first entry)
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                     Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-322654/28.
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                                                                                                             09-NOV-1998
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                                                                              AAW62760;
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AAM82654
                   ESULT 30
                                  AW62760
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02-OCT-2000; 2000US-0236802P.
02-OCT-2000; 2000US-0236802P.
02-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-023935P.
20-OCT-2000; 2000US-023937P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-024651P.
17-NOV-2000; 2000US-024651P.
17-NOV-2000; 2000US-024651P.
17-NOV-2000; 2000US-024651P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024921P.
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0; 2000US-0249244P.
0; 2000US-0249245P.
0; 2000US-0249245P.
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17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249217P.
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17-NOV-2000; 2
17-NOV-2000; 2
11-DEC-2000; 2
01-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
06-DEC-2000; 2
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06-DEC-2000; 2
06-DEC-2000; 2
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17-NOV-2000
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Barash SC, Ruben SM; WPI; 2001-483426/52 Rosen CA,

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) and acid sequences given in AAM62170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polymucleotides may be used in the prevention, diagnosis and proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to cupplement the patients own production of (1). Additionally, (1) polymucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 cancers and cancer metastesses of haematopoietic-darived cells. AAK64703 cancers and cancer metastesses of haematopoietic antiden genomic to AAK87694 represent human immune/hamatopoietic antiden genomic sequences from the present invention. AAK64921 to AAK67950 and AAM82169 sequences trom the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor; immunomodulatory, cancer, leukaemia, nervous system disorders, arthritis, inflammation.
                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                            Claim 11; SEQ ID NO 10247; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 4; Length 32; ilarity 100.0%; Pred. No. 4.3e+02; Conservative 0; Mismatches 0; Indels
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18-MAY-2000; 2000US-00577409.
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es 4; Conserv
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N-PSDB; AAK55435
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Best Local S
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AAO09024
ID AAO090
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The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to prytokine, cell publication or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The peptide therapy, waccines or polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, mmunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity,inhibin activity and may be useful in the diagnosis and/or treatment of cancer, laukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences

Sequence 33 AA;

Gaps ö 95.0%; Score 19; DB 4; Length 33; 100.0%; Pred. No. 4.4e+02; tive 0; Mismatches 0; Indels 4; Conservative Query Match Best Local Similarity Matches 4; Conserva' 2 VAEF 5 3 VAEF 6 ⋩

AAR77953 standard; peptide; 35 AA. 4AR77953 

09-OCT-1996 (first entry) AAR77953;

Antigenic Tbp2 peptide TBP2-21

Tbp1, Tbp2, transferrin receptor operon, vaccine, antigen, non-typable strain, Haemophilus influenzae, meningitis.

Synthetic.

WO9513370-A1

18-MAY-1995.

93US-00148968. 08-NOV-1993;

94WO-CA000616.

07-NOV-1994;

(CONN-) CONNAUGHT LAB LTD.

Loosmore S, Harkness R, Schryvers A, Chong P, Gray-Owen S; Yang Y, Murdin A, Klein M;

WPI; 1995-194089/25.

Nucleic acids encoding Haemophilus transferrin receptor - used to develop prods for detection and in diagnosis, prevention and treatment of prods for detection an Haemophilus infection.

Example 16; Page 72; 231pp; English.

AAR77933-969 are predicted antigenic peptides derived from conserved regions of the ThD2 protein from H. influenzae strains Bagan, MinnA, DL63 and non-typable strain PAK12085. The transferrin receptor (IfR) operon consists of two genes (Tbp1 and Tbp2) arranged in tandem and which are transcribed from a single promoter. H. influenzae IfR is Iron- and/or haemin-regulated and a putative fur-binding site has been identified upstream of tbp2. Antibodies blocking this binding site may prevent bacterial growth. Fragments of the FfR (or its genes) are useful in vaccines to provide protection against, e.g. bacterial meningitis. An advantage of using the IfR is that it shares homology with IfR of other

H. influenzae strains including non-typable strains. According to the specification the present sequence shows residues 449-484 of Tbp2 from the H. influenzae strain Eagan ន្តដូន្ធន

Sequence 35 AA;

ö Gaps .. 0 95.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 4.7e+02; 0; Indels 100.0%; Pred. No. 4; Conservative Best Local Similarity Matches 4; Conserv 2 VAEF 5 Query Match

RESULT 34

14 VAEF 17

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**AAW46146** 

AAW46146 standard; protein; 35 AA.

05-MAY-1998 (first entry)

AAW46146;

; 0

Predicted antigenic Tbpl peptide TBP2-21.

Transferrin receptor; Haemophilus influenzae type b; iron; human transferrin; iron source; antibody; bacterial growth; vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2.

Haemophilus influenzae. Synthetic

WO9640929-A2. 

19-DEC-1996

96WO-CA000399. 07-JUN-1996;

95US-00483577. 96US-00649518. 07-JUN-1995; 17-MAY-1996;

(CONN-) CONNAUGHT LAB LTD.

Schryvers AB, Chong P, Gray-Owen Klein MH; Harkness RE, Loosmore SM, Harkner Yang Y, Murdin AD,

WPI; 1997-052329/05.

Haemophilus truncated transferrin receptor protein analogue, Tbp2 - uto induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.

Example 16; Page 70; 228pp; English.

protein of Haemophilus influenzae type b. The deduced amino acid receptor, of which They is also a subunit. The deduced amino acid receptor, of which They is also a subunit. The deduced amino acid sequences of They and They were compared, and regions of conservation identified. The above peptides are derived from these regions, the present peptide being derived from residues 449-484. Iron is an essential quirient for the growth of these bacteria, and they can utilise human current for the growth of these bacteria, and they can utilise human cransferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The transferrin receptor to its iron source prevent bacterial growth. The transferrin receptor, or fragments, therefore, are good vaccine candidates. An immunogenic composition comprising for encoding) the immunogenic truncated analogue is also useful as an antigen in immunosasays for the detection of Haemophilus transferrin receptor antibodies, while the nucleic acid molecule can be used as a nutigen bybridisation probe for the detection of other transferrin receptor genes

Sequence 35 AA;

Human; aquaporin-1; AQP-1; water channel protein; regulation; osmotic change; erythrocyte; dryness; blindness; hydration; asthma;

secretion.

Human aquaporin-1 NH2-terminal amino acid sequence CHIP28.

14-JUL-1998 (first entry)

AAW55788;

AAW55788 standard; peptide; 35 AA.

RESULT 36

AAW55788

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
                                                                            Gaps
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          Length 35;
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                                                                     0; Indels
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h
Similarity 100.0%; Pred. No. 4.7e+02;
4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H. influenzae antigenic Tbp2 peptide TBP2-21.
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                                                                                                                                                                                                                                                                                                                                                                        AAY51751 standard; protein; 35 AA.
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94US-00337483.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
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Best Local Similarity
Than 4; Conservat
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   Query Match
Best Local Similarity
Matches 4; Conserv
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08-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis.
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                                                                                                                                                                                                                                                                                                       RESULT 35
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AAY
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Polynuclectide(s) encoding water channel protein Aquaporin-1 - are useful for recombinant production of protein for activity studies.
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                                                                                                                                                                                                                          /note= "not specified but is given as Ser in the full
length protein given in AAW55786"
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                                                                                                                                                                                                                    'label= Unknown
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Misc-difference
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                                                                                                                                                             Homo sapiens.
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24-FEB-1995;
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Matches
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Gaps

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14 VAEF 17

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                                                                                                                                                                                                                                                                                           Purification of recombinant Haemophilus transferrin-binding protein solubilising inclusion bodies separated from cell lysate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; aquaporin-5; AQP5; AQP1; transmembrane water channel protein; major intrinsic protein; MIP; CHIP28.
                                                                                                                                                                                                                             Chong
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                                                                                                                                                                                                                              Yang Y,
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Similarity 100.0%; Pred. No. 4.7e+02;
4; Conservative 0; Mismatches 0; Indels
        tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis; passive immunisation; transferrin receptor operon.
                                                                                                                                                                                                                                Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human aquaporin-1 (CHIP28) N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                  Example 16/17; Column 37-38; 261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "unspecified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW94320 standard; peptide; 35 AA
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93US-00175116.
94US-00337483.
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                                                                                                                                                                                                     (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                              Gray-Owen S, Klein M,
Murdin A, Schryvers A;
                                               Haemophilus influenzae
                                                                                                                                                                                                                                                                   WPI; 1998-100410/09
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 35 AA;
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29-DEC-1993;
08-NOV-1994;
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                                                                                                                         1995;
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                                                                        US5708149-A
                                                                                                  13-JAN-1998
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Matches
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5 (AQPS). The polymucleotide encoding AQPS is useful for producing
recombinant AQPS, which can be incorporated into proteoliposomes or cell
membrane vesicles which are able to be used in screening assays for water
channel agonists or antagonists. The present sequence represents the N-
terminal peptide from AQP1 (also called CHIP28), from an example of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies specific for transferrin receptor proteins of Haemophilus
influenzae, useful for treating otitis media, epiglottitis, pneumonia and
                                                                                                           DNA encoding aquaporin-5 water channel protein - useful for producing
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel antibodies (or monospecific antisera) specific for single transferrin receptor proteins (or immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibacterial; antiinflammatory; auditory; respiratory; antibody; antiserum; transferrin receptor; immunogen; epitope; otitis media; bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.
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                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 4.7e+02; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H. influenzae transferrin receptor Tbpl epitope TBP2-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gray-Owen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Col 37-38; 252pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY80448 standard; peptide; 35 AA.
                                                                                                                                                    Example 2; Col 20; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00148968.
93US-00175116.
95US-00337483.
 92US-00930168.
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                         UNIO ) UNIV JOHNS HOPKINS
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Schryvers A;
                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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                                                                                                                             recombinant protein
                                                                                WPI; 1999-152100/13
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                  present invention
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                                                                                                                                                                                                                                                                                             Sequence 35 AA;
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29-DEC-1993;
08-NOV-1995;
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17-AUG-1992;
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The present sequence represents a Staphylococcus aureus protein, that, based on homology with a Bacillus subtilis protein, is believed to be a probable UDP-N-acetylglucosamine 1-carboxyvinyltransferase (encylpyruvate transferase). The DNA sequence was isolated from a library of clones of S. aureus WCH 29 in Escherichia coli. The DNA sequence can be used in the construction of riboxymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
              corresponds to an epitope from the H. influenzae transferrin receptor protein TDp2. The antibodies may be used for preventing and treating infections and disorders caused by H. influenzae, including bacterial meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis. The antibodies may also be used detect the presence of H. influenzae proteins in samples according to standard methodologies (e.g. enzyme linked immunosorbant assay (ELISA)) and hence diagnose infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used to
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - use isolate antimicrobial compounds, and in vaccines against S. aureus
fragment) from strains of Haemophilus influenzae. This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knowles DJC, Nicholas RO;
, Ward JM;
                                                                                                                                                                                     95.0%; Score 19; DB 3; Length 35; 100.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hodgson JE, Ku
Rosenberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "not specified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       AAW27782 standard; protein; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 272; 989pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                            4; Conservative
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Reichard RW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    toxic shock syndrome
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N-PSDB; AAT83751.
                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                               14 VAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Misc-difference
                                                                                                                                                                                                                                                              2 VAEF 5
                                                                                                                                                         Sequence 35 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9730070-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1998
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Pratt JM,
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AAW27782
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produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome
                                                                                                                                                                                                                                                                                                             Human; nootropic, neuroprotective, cytostatic; dermatological; virucide; immunosuppressive; antihatlammatory; anti-HIV; antibaterial; vulnerary; antiparkinsonian; antiaickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antithatergic; antidiabetic; erebroprotective; antiinflammatory; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                        Gaps
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                                                                                DB 2; Length 36;
4.8e+02;
hes 0; Indels
                                                                                                                                                                                                                                                                                         Human excretory related polypeptide SEQ ID NO 570.
                                                                                 95.0%; Score 19; DB 100.0%; Pred. No. 4.8
                                                                                                                                                                                                                  AAM99833 standard; protein; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0190076P.
2000US-0198123P.
2000US-0205515P.
2000US-0209467P.
2000US-0214886P.
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2000US-0224519P.
2000US-0225213P.
2000US-022514P.
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2000US-0186350P.
2000US-0189874P.
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                                                                                                                                                                                                                                                                  07-JAN-2002 (first entry)
                                                                                                        4; Conservative
                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   excretory system.
                                                                                                                                  2 VAEF 5
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                                                             Seguence 36 AA;
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16-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2000;
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28-JUN-2000;
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14-AUG-2000;
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2000US-0236802P.
2000US-0237037P.
2000US-0237039P.
2000US-0237040P.
2000US-023933EP.
2000US-023933EP.
2000US-023933EP.
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2000US-0246475P.
2000US-0246477P.
2000US-0246477P.
2000US-0246477P.
2000US-0246478P.
2000US-024653P.
2000US-0246528P.
2000US-024652FP.
2000US-024652FP.
2000US-024652FP.
18-Aug-2000)
22-Aug-2000)
22-Aug-2000)
23-Aug-2000)
23-Aug-2000)
21-SEP-2000)
21-SEP-2000)
22-Aug-2000)
23-Aug-2000)
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28-SEP-2000)
28-SEP-2000)
29-SEP-2000)
20-SEP-2000)
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The invention relates to novel excretory system related human polymuclectides (AA199567-AA199503) and the encoded proteins (AAM99594-CO polymuclectides (AA199567-AA199503) and the encoded proteins (AAM99594-CO polymuclectides (AA199567-AA199503) and the encoded proteins (AAM99594-CO conditions e.g. by protein or gene therapy, espeically disorders related to the excretory system. The genes are isolated from a range of human tissue disclosed in the specification. The nucleic acids, proteins, crisques disclosed in the specification. The nucleic acids, proteins, crevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal prevention of: (a) cancer, luver, lung, or uroganital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, cheumatoid arthrities and ulcerative colitis; (c) cardiovascular disorders such as wrocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases cuch as viral bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fifty. Wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding excretory system antigen is in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 570; 574pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Barash SC, Ruben SM
                              2000US-0249208P-
2000US-0249210P-
2000US-0249211P-
2000US-0249211P-
2000US-0249213P-
2000US-0249213P-
2000US-0249214P-
2000US-0249214P-
2000US-0249214P-
2000US-0249214P-
2000US-0249218P-
2000US-0249248P-
2000US-0249248P-
2000US-0249248P-
2000US-0249248P-
2000US-0249248P-
2000US-0249248P-
2000US-0249248P-
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2000US-0249248P-
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2000US-024929P
2000US-025900P
2000US-025030P
2000US-0250391P
2000US-025039P
2000US-025039P
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2000US-0251869P.
2000US-0251989P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-465569/50.
N-PSDB; AAI98806.
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Sequence 37 AA;

Gaps .. o 11arity 100.0%; Score 19; DB 4; Length 37; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 4; Conserv

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Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic; antipheroliferative; Cytostatic; cardiant; vasotropic; cerebroprotective; nortoropic; cerebroprotective; nortoropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; antiallergic; hepatocropic; antidiabetic; antillergic; hepatocropic; antidiabetic; antillergic; antidiammatory; antiulcer; vulnerary; anticonvulsant; antiparasitic; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection.
                                                                                                                                                                                                                 Human kidney related polypeptide SEQ ID NO 517
                                                                                                      AAM42648 standard; protein; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2000; 2000US-0179065P.
24-FEB-2000; 2000US-0118062BP.
24-FEB-2000; 2000US-01184664P.
02-MAR-2000; 2000US-01184664P.
16-MAR-2000; 2000US-01189874P.
17-MAR-2000; 2000US-0198174P.
18-MAR-2000; 2000US-0198174P.
19-MAY-2000; 2000US-011886P.
26-JUN-2000; 2000US-021486P.
11-JUL-2000; 2000US-021486P.
11-JUL-2000; 2000US-021486P.
11-JUL-2000; 2000US-021486P.
11-JUL-2000; 2000US-021664P.
11-JUL-2000; 2000US-021664P.
11-JUL-2000; 2000US-021664P.
11-JUL-2000; 2000US-021664P.
11-JUL-2000; 2000US-021866P.
14-JUC-2000; 2000US-022514P.
14-JUC-2000; 2000US-022516P.
14-JUC-2000; 2000US-022516P.
14-JUC-2000; 2000US-022516P.
14-JUC-2000; 2000US-022516P.
14-JUC-2000; 2000US-022516P.
14-JUC-2000; 2000US-022514P.
11-JUC-2000; 2000US-022516P.
11-JUC-2000; 2000US-022518P.
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                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200155323-A2.
VAEF
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                                                                                                                                                                             22-OCT-2001
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                   14
                                                                                                                                          AAM42648;
                                                                                       AAM42648
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17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

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01-NOV-2000)
08-NOV-2000)
                                                                       25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
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02-OCT-2000;
02-OCT-2000;
                                                                                                                                13-0CT-2000,
20-0CT-2000,
20-0CT-2000,
20-0CT-2000,
20-0CT-2000,
20-0CT-2000,
20-0CT-2000,
20-0CT-2000,
                                                                                   27-SEP-2000;
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The invention relates to novel kidney related polymuclectides (AAJ62971-AAJ63993) and the encoded polypeptides (AAM2417-AAJ63691) collectively known as kidney antigens and the use of such kidney antigens for cancer metastases. The kidney, especially kidney cancer and kidney cancer metastases. The polymuclectides and proteins are also useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and ant) gancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urgoeintal, (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic ansemia, autoimmune thyroiditis, diabetes mellitus Crohn's disease, multiple sclerosis, rheumatoid any myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy, and (f) infectious diseases such as viral, controlic form part of the printed specification, but was controlic formet directly from WIPO at
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17-NOV-2000) 2000US-0249245P.
17-NOV-2000) 2000US-0249264P.
17-NOV-2000) 2000US-0249264P.
17-NOV-2000) 2000US-0249297P.
17-NOV-2000) 2000US-0249299P.
17-NOV-2000) 2000US-0249299P.
17-NOV-2000) 2000US-0249300P.
01-DEC-2000) 2000US-025198P.
05-DEC-2000) 2000US-025198P.
05-DEC-2000) 2000US-025198P.
06-DEC-2000) 2000US-025186P.
08-DEC-2000) 2000US-025186P.
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N-PSDB; AA163202.
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Best Local Similarity
Matches 4; Conserv
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AM17544
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The present invention relates to human single exon nucleic acid probes (SERP): see AAIIOOGS-AAISO459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical acheer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; microarray; single exon probe; gene expression; breast; disease;
             Peptide #3978 encoded by probe for measuring cervical gene expression.
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                                        Probe, human, microarray, gene expression, cervical epithelial cell;
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                                                                                                                                                                                                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB31362 standard; peptide; 43 AA.
                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                 2000US-0180312P.
2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
                                                                                                                                                                     30-JAN-2001; 2001WO-US000670.
                                                                                                                                                                                                                                                                        27-SEP-2000; 2000US-0236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                  Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 VAEF 43
                                                       cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                               WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157271-A2
                                                                                                                                                                                                                                             33-AUG-2000;
21-SEP-2000;
                                                                                    Homo sapiens.
                                                                                                                                                                                                                                30-JUN-2000;
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                                                                                                                                                                                                    04-FEB-2000;
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                                                                                                                                         09-AUG-2001.
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Gaps

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probes of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They proposing breast disease. Gene expression analysis is useful for prognosing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag information from genomic sequence. The present sequence is a peptide encoded by a single exon mucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed sequence.
                                                                                                                                                                                                                                                                                                                                  New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 14330; 327pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                        26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-ACG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                   30-JAN-2001; 2001WO-US000662
                                                       2000US-0180312P
                                                                                                                                                                                                                                                          Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                WPI; 2001-496933/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43 AA;
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95.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02; ive 0; Mismatches 0; Indels
                     Best Local Similarity 100.
Matches 4; Conservative
                                                                             2 VAEF 5
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ABB21904 standard; protein; 43 AA. ABB21904; RESULT 4: XSXBXBXBXGXGX

Protein #3903 encoded by probe for measuring heart cell gene expression. (first entry) 23-JAN-2002

Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.

Homo sapiens

WO200157274-A2

09-AUG-2001

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see PARA1305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                            Claim 15; SEQ ID NO 23674; 530pp; English.
                                                                                                                                                                                                        Chen W, Rank DR
                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                 21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                2000US-00608408
2000US-00632366
30-JAN-2001; 2001WO-US000666
                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                      WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43 AA;
                                               26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                                                                                             hearts
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Gaps ö 95.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02; tive 0; Mismatches 0; Indels Similarity 100.0%; 4; Conservative 0 Query Match Best Local Similarity Matches 4; Conserv

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ò g ABG51414

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Human liver peptide, SEQ ID No 30062. ABG51414 standard; peptide; 43 AA. (first entry) 25-FEB-2003 ABG51414;

Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease. , 2000US-0180312P. , 2000US-0204456P. , 2000US-0068408 , 2000US-00632366. , 2000US-0234687P. , 2000US-0234687P. 30-JAN-2001; 2001WO-US000664 WO200157273-A2 26-MAY-2000; 30-JUN-2000; 03-AUG-2000; 21-SEP-2000; 27-SEP-2000; 04-OCT-2000; Homo sapiens 04-FEB-2000; 09-AUG-2001 

Chen W, Rank DR,

Hanzel DK,

Claim 27; SEQ ID NO 30062; 658pp; English AAM05214 standard; protein; 43 AA. 26-MAY-2000; 2000US-0207456P. 30-JUN-2000; 2000US-0069408. 03-AUG-2000; 2000US-00632366. 27-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-0234559P. 04-OCT-2000; 2000GB-00024263. (MOLE-) MOLECULAR DYNAMICS INC (MOLE-) MOLECULAR DYNAMICS INC 29-JAN-2001; 2001WO-US000661 Query Match Best Local Similarity 100.00 4; Conservative WPI; 2001-476286/51 WPI; 2001-488898/53 WO200157270-A2 Homo sapiens 04-FEB-2000; 09-CT-2001 Sequence 43 09-AUG-2001 AAM05214; Penn SG, Penn SG, ESULT 47 **RANHRANHHWWNDDDDDDDDDDDDDDDDD** ج<u>خ</u> Ω.

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(first entry)

Chen W, Rank DR;

Hanzel DK,

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The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one auch probes. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention is concerned with producing vaccines against negative stranded RNA viruses. These viruses include measles, respiratory syncytial virus (RSV) and parainfluenza virus (PIN) in particular. The method of the invention comprises the production of a mutated form of the virus which attenuates the strain and enables it to be used as a vaccine. The present sequence comprises a partial viral protein sequence
Novel single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing attenuated negative stranded RNA virus vaccines from cloned gequences, useful for immunizing against e.g. respiratory syncytial virus, human parainfluenza virus, Sendai virus Newcastle disease virus mungs virus and measles virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Negative stranded RNA virus; vaccine; attenuated virus; RSV; PIV; measles; respiratory syncytial virus; parainfluenza virus.
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100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSV partial protein sequence SEQ ID NO: 26.
                                                                  Claim 27; SEQ ID NO 13954; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 62; 137pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB27178 standard; protein; 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2000; 2000WO-US009695.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-687044/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 VAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 43 AA;
                         a human breast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB27178;
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Matches
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                                                                                                                                                                                                                                                                             The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, myperial proproteinmenta, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. Add47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from WIPO at the printed specification ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02; tive 0; Mismatches 0; Indels
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(first entry)

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Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                             Peptide #5084 encoded by human foetal liver single exon probe.
                      ABB37578 standard; peptide; 48 AA.
                                                                                                                                                                   WO200157277-A2
                                                                                                                                             Homo sapiens
                                                                     04-FEB-2002
                                                                                                                                                                                           09-AUG-2001
                                              ABB37578;
RESULT 50
ABB37578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to human single exon nucleic acid probes (SENP: see AA110068-AA128459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or eraging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                 Peptide #4975 encoded by probe for measuring cervical gene expression.
                                              Gaps
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                                                                                                                                                                                                                                                        Probe; human; microarray; gene expression; cervical epithelial cell;
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100.0%; Pred. No. 6.6e+02;
rative 0; Mismatches 0; Indels
                      Length 47;
                                              Indels
                      95.0%; Score 19; DB 3; Lr
100.0%; Pred. No. 6.4e+02;
iive 0; Mismatches 0;
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                                                                                                                                                        AAM18541 standard; protein; 48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0063266.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                        (first entry)
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                                              4; Conservative
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Best Local Similarity
Matches 4; Conserv
                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                              34 VAEF 37
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Sequence 47 AA;
                                                                                                                                                                                                                                                                    cervical cancer
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                                                                                                                                                                                                                                                                                                                  WO200157278-A2.
                                                                                                                                                                                                                                                                                              Homo sapiens.
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human feetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #5033 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 30213; 639pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
95.0%; Score 19; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
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                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                  30-JUN-2000; 2000US-00608408.
21-SEP-2000; 2000US-0063356.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236559P.
04-OCT-2000; 2000GB-00024263.
30-JAN-2001; 2001WO-US000669
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                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483447/52
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                                                  04-FEB-2000;
26-MAY-2000;
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2 VAEF 5

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                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein #4867 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression; heart; microarray; vascular system; vascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 4; Length 48; 100.0%; Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ...
'''A 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 31265; 654pp; English
                                                                                                                                                                                                                                                                                                                                                             Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon n
gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB22868 standard; protein; 48 AA.
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2000US-00608408.
2000US-0234687P.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
                                                                                                                                                                                                03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0235599.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                        2000US-0207456P.
2000US-00608408.
                                                                                     30-JAN-2001; 2001WO-US000663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            congenital heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiovascular
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WO200157272-A2
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                        26-MAY-2000;
                                                                                                                                  04-FEB-2000;
                                          09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                  The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see $A$21535-A$441906). The present sequence is a procein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pcr_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bone marrow expressed probe encoded protein SEQ ID NO: 30993
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                                                                                                                                             Claim 15; SEQ ID NO 24638; 530pp; English
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                                       Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM70687 standard; protein; 48 AA.
            (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000; 2000US-0180312P.
26-WAY-2000; 2000US-0207456F.
30-JUN-2000; 2000US-00609408.
Q3-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
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Best Local Similarity 100.
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                                         Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488900/53.
                                                                    WPI; 2001-488899/53
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 48 AA;
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Gaps

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0; Indels Length 48;

DB 4; L

Query Match 95.0%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 6.6 Matches 4; Conservative 0; Mismatches

Sequence 48 AA;

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Gaps

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Length 48; Indele

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but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences

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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59390 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification
                                                          probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing
                                            The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
         Example 4; SEQ ID NO 30993; 658pp + Sequence Listing; English
                                                                                                                                                                                                           95.0%; Score 19; DB 4; Let 100.0%; Pred. No. 6.6e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           claim 27; SEQ ID NO 31037; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human liver peptide, SEQ ID No 31037.
                                                                                                                                                                                                                                                                                                                                                                                                                ABG52389 standard; peptide; 48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0207456F.
30-UJN-2000; 2000US-00608408
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000US-023659P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                             Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                      2 VAEF 5
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                                                                                                                                                                            Sequence 48 AA;
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llarity 100.0%; Pred. No. 6.6e+02;
Conservative 0; Mismatches 0; Indels
Claim 27; SEQ ID NO 14847; 322pp; English
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ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
ses 4; Conserv
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Matches
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The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actionages include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel single exon nucleic acid probe used to measuring gene expression in a human breast.
                                                                                                                                                 Probe, human; breast disease, breast cancer, development disorder;
inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                  Peptide #4789 encoded by probe for measuring breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR;
                            AAM06107 standard; protein; 48 AA.
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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                                                                                       (first entry)
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                       09-OCT-2001
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                                                           AAM06107;
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RESULT 55
                  AAM06107
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AA005247;

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2 VAEF

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The invention relates to human polymuclectides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetrides are useful in gene therapy, vaccines or peptide therapy. The polymetrides are various cytokine-like activities, e.g. stem cell growth factor activity, humanomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 24457.
                                                                                                                                                                                             AA010565 standard; protein; 53 AA
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18-MAY-2000; 2000US-00577409.
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N-PSDB; AAI90496.
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VAEF 6
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                                                                                                                                                             AO10565
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The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to protokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polymetides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiti, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                           Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia, nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 19139; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 4; Length 53; 100.0%; Pred. No. 7.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen SEQ ID NO:14983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM87390 standard; protein; 56 AA.
                                                                Human polypeptide SEQ ID NO 19139.
                                                                                                                                                                                                                                                                                                                                                                                                             Fang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                        28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                         26-FEB-2001; 2001WO-US004927
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                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-514838/56
                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAI85178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 53 AA;
                                                                                                                                                                                                                       WO200164835-A2
                                                                                                                                                                                        Homo sapiens
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                                06-NOV-2001
                                                                                                                                                                                                                                                        07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 58
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Homo sapiens

AAO05247 standard; protein; 53 AA.

ESULT 57

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Gaps ô

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31-JAN-2000; 2000US-0179065P.

24-FRB-2000; 2000US-0186536P.

22-FRB-2000; 2000US-0186350P.

16-MAR-2000; 2000US-0186350P.

16-MAR-2000; 2000US-0189874P.

17-MAR-2000; 2000US-019874P.

18-AFR-2000; 2000US-019874P.

11-JUL-2000; 2000US-019874P.

11-JUL-2000; 2000US-019874P.

11-JUL-2000; 2000US-019874P.

11-JUL-2000; 2000US-019874P.

11-JUL-2000; 2000US-019878P.

11-JUL-2000; 2000US-0117488FP.

11-JUL-2000; 2000US-0215115P.

07-JUL-2000; 2000US-021648FP.

11-JUL-2000; 2000US-021648FP.

11-JUL-2000; 2000US-021648FP.

11-JUL-2000; 2000US-021648FP.

11-JUL-2000; 2000US-021748FP.

11-JUL-2000; 2000US-021648FP.

14-JUL-2000; 2000US-021748FP.

14-JUL-2000; 2000US-021648FP.

14-JUL-2000; 2000US-021648FP.

14-JUL-2000; 2000US-022514P.

14-JUC-2000; 2000US-0231414P.

14-SEP-2000; 2000US-0231414P.

14-SEP-2000; 2000US-0231341P.

14-SEP-2
                                                                     2001WO-US001354
            WO200157182-A2
                                                                     17-JAN-2001;
                                          09-AUG-2001
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2000US-0236327P 2000US-0236367P 2000US-0236369P 2000US-0237037P 2000US-0237037P 2000US-0237037P 2000US-0237037P 2000US-0237037P 2000US-0237037P 2000US-0237038P 2000US-0237038P 2000US-0237038P 2000US-0241886P 2000US-024861P 2000US-024821P 2000US-024828P 2000US-025186P 2000US-025186P 2000US-025186P 2000US-0254097P 2001US-0259678P 29-SBP-2000; 29-SBP-2000; 29-SBP-2000; 29-SBP-2000; 29-SBP-2000; 29-SBP-2000; 29-SBP-2000; 29-SBP-2000; 29-SBP-2000; 20-SBP-2000; 20-SB 08-DEC-2000; 2 11-DEC-2000; 2 0S-JAN-2001; 2 

HUMAN GENOME SCI

(HUMA-)

us-09-594-978a-3.rag

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAW82170 to AAW91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metaateses of haematopoietic-delived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK5950 and AAM82169 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human matrix metalloproteinase 7 cleavage region peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                     claim 11; SEQ ID NO 14983; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 4; Length 56; 100.0%; Pred. No. 7.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.
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Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-AUG-2001; 2001US-0312726P.
21-DEC-2001; 2001US-00032376.
21-MAY-2002; 2002US-00153185.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
Barash SC,
                                                                           WPI; 2001-483426/52
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Best Local Similarity
                                                                                                                 N-PSDB; AAK60171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56 AA;
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Rosen CA,
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Gaps . 0

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                                                                                                                                The present invention describes an anti-angiogenic composition (1) for inhibiting expression of vascular endothelial growth factor (VEGF). (1) comprises an effective amount of a peptide inhibitor of matrix metalloproteinase (WMP), where the peptide inhibit the expression of VEGF. (1) has cytostatic, vulnerary, cardiant, cerebroprotective, antidiabetic, ophthalmological and dermatological activities. (1) used for inhibiting expression of VEGF, and so can be used for inhibiting growth of tumours and diminishing tumours size. The tumour can be metastatic, non-metastatic, vascularised, non-vascularised, hard or metastatic, non-metastatic, vascularises including wounds, surgical incisions, chronic wounds, heart diseases and stroke. (1) is also useful
                                                                                                                                                                                                                                                                                                                                   for treating disorders characterised by excessive angiogenesis e.g. macular degeneration and diabetic retinopathy. The present sequence represents a human MMP cleavage region peptide, which is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; peptide inhibitor; matrix metalloproteinase-7; MMP-7; cleavage region; proenzyme form; cellular proliferation; fibroblast; keratinocyte; healthy skin development; wound healing; scarring; skin tone; wrinkle; anti-aging; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide inhibitor of proteinase activity of matrix metalloproteinases, e.g. matrix metalloproteinase-2, useful for stimulating cellular proliferation of fibroblasts or keratinocytes.
                                                 vascular
                              Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 6; Le
100.0%; Pred. No. 7.8e+02;
iive 0; Mismatches 0;
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                                                                                                         Claim 17; Page 15; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 16; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG76312 standard; protein; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-2001; 2001US-0312726P.
21-DEC-2001; 2001US-00032376.
21-MAY-2002; 2002US-00153185.
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WPI; 2003-381408/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 56 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 60
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The present invention relates to peptide inhibitors of metalloproteinases (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have peptide sequences related to the cleavage regions of the proenzyme forms of the MMPS. The peptide inhibitors are useful for stimulating callular proliferation of fibroblasts or keratinocytes, promoting healthy skin development, treating wounds, preventing scarring, improving skin tone, reducing wrinkling and for simulating the development of smooth, healthy skin. The peptide inhibitors are useful as anti-aging and wound healing compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs
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Sequence 56 AA;

Gaps ; 0 Length 56; Query Match 95.0%; Score 19; DB 6; Length 56; Best Local Similarity 100.0%; Pred. No. 7.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels 31 VAEF 34 2 VAEF 5 ઠે g

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RESULT 61

AAW55888 standard; protein; 58 AA.

AAW55888;

(first entry) 22-JUL-1998 

Rat PC12.

Rat; telomerase; human; cancer; screening; inhibitor; elucidation; detection; probe; diagnosis; cell growth; ageing.

Rattus sp.

WO9807838-A1

26-FEB-1998,

97WO-JP002904. 21-AUG-1997;

96JP-00219761. 97JP-00018878. 21-AUG-1996; 17-FEB-1997;

(MITU ) MITSUBISHI CHEM CORP.

Takahashi K, Fujino Y, Harada N; Ishikawa F, Nakamura H,

Disclosure; SEQ ID NO 9690; 1037pp; English.

WPI; 1998-169149/15. N-PSDB; AAV25990 Telomerase protein of higher animals and humans and gene encoding it - for use in diagnosis of cancer, screening of telomerase inhibitors and elucidation of biological control mechanisms.

Example 1; Page 69-70; 105pp; Japanese.

The present sequence represents rat PC12 which is used in an example of the present invention which describes protein components of telomerase. The DNA or RNA encoding the telomerase protein component or its fragments can be used as a nucleotide probe for the detection of cancer cells and for diagnosis of cancer. Potential telomerase inhibitors can be screened by measuring their effect on the assay of the active form in cells or tissues. The polypeptide and DNA coding for it can be used in the elucidation of biological control mechanisms of, e.g. cell growth or ageing and of the mechanisms of cancer development.

Sequence 58 AA;

Query Match

DB 2; 95.0%; Score 19;

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                                                                                                                                                                                                      Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperpoilferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human polypeptides and polymucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
              ċ
 ; Pred. No. 8.1e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                     Human ORFX protein sequence SEQ ID NO:9690.
                                                                                                                 ABP04854 standard; protein; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
  100.08;
                                                                                                                                                             24-JUN-2002 (first entry)
              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-106308/14.
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                        myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABN20606.
                                                         49 VAEF 52
                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                    WO200192523-A2.
                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                       ABP04854;
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABNIS762 to ABNIZ725 encode the human ORFX proteins are useful for in the specification). ABNIS762 to ABNIZ725 encode the human ORFX proteins are useful for treating or preventing a pathology associated with an ORFX passociated disorder in humans, and in the manufacture of a medicament for treating of syndrome associated with ORFX associated disorder. ORFX polynucleotide syndrome associated in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthitis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders, infectious controlled accorders such and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthitis, autoimmune infilammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not

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990S-0137724P.
990S-0137724P.
990S-0138647P.
990S-0138647P.
990S-0139452P.
990S-014033P.
990S-014035P.
990S-014035P.
990S-014035P.
990S-014433P.
990S-0145218P.
990S-0145218P.
990S-0145218P.
990S-0145218P.
990S-014531P.
990S-014531P.
990S-014531P.
990S-014531P.
990S-014531P.
990S-014531P.
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05-AUG-1999;
05-AUG-1999;
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
                                                                                                                                                                                                                                                                                                                            24-JUN-1999;
28-JUN-1999;
29-JUN-1999;
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                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
    form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                              Gaps
                                                                                              ö
                                                               Query Match

Best Local Similarity 100.0%; Pred. No. 8.18+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 77787.
                                                                                                                                                                                                               AAG60085 standard; protein; 59 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0121825P.
99US-0123180P.
99US-0125788P.
99US-012624P.
99US-012624P.
99US-012462P.
99US-012462P.
99US-012824P.
99US-013091P.
99US-013091P.
99US-0131449P.
99US-0131449P.
99US-0131449P.
99US-0131449P.
99US-0132486P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                  18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                               30 VAEF 33
                                                                                                                     2 VAEF 5
                                            Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-ARR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
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14-MAX-1999)
14-MAX-1999)
14-MAX-1999)
19-MAX-1999)
20-MAX-1999
21-MAX-1999
24-MAX-1999
25-MAX-1999
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01-JUN-1999;
03-JUN-1999;
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                                                                                                                                                                                                                                         AAG60085;
                                                                                                                                                                                     ESULT 63
AG60085
      0.0 \times 0
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R 66-MAC-1999; 9918-0-144102P.
PR 102-MAC-1999; 9918-0-144102P.
PR 102-MAC-1999; 9918-0-144102P.
PR 102-MAC-1999; 9918-0-144102P.
PR 113-MAC-1999; 9918-0-144626P.
PR 113-MAC-1999; 9918-0-144626P.
PR 113-MAC-1999; 9918-0-144462P.
PR 113-MAC-1999; 9918-0-144462P.
PR 123-MAC-1999; 9918-0-144462P.
PR 22-MAC-1999; 9918-0-144922P.
PR 22-MAC-1999; 9918-0-144922P.
PR 22-MAC-1999; 9918-0-144922P.
PR 22-MAC-1999; 9918-0-14992P.
PR 22-MAC-1999; 9918-0-15066P.
PR 22-MAC-1999; 9918-0-15061P.
PR 22-MAC-1999; 9918-0-15061P.
PR 22-MAC-1999; 9918-0-16061P.
PR 23-MAC-1999; 9918-0-16061P.
PR 23-MAC-19
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 Gaps
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   Indels
                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 78631.
   ;
   0; Mismatches
                                                                                                                                   AAG60683 standard; protein; 59
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99US-0123180P.
99US-0125788P.
99US-01264P.
99US-01264P.
99US-0127462P.
99US-0128234P.
99US-0128234P.
99US-013081P.
99US-013081P.
99US-01324407P.
99US-01324407P.
99US-0132482P.
99US-0134218P.
99US-013422P.
99US-013522P.
99US-0137724P.
99US-0137724P.
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                                                                                                                                                                                             18-OCT-2000 (first entry)
    4; Conservative
                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                          45 VAEF 48
                               2 VAEF 5
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05-MAY-1999

06-MAY-1999

06-MAY-1999

11-MAY-1999

14-MAY-1999

14-MAY-1999

14-MAY-1999

14-MAY-1999

19-MAY-1999

19-MAY-1999

21-MAY-1999

21-MAY-1999

22-MAY-1999

22-MAY-1999

23-MAY-1999

24-MAY-1999

25-MAY-1999

25-MAY-1999

25-MAY-1999

27-MAY-1999

27-MAY-1999
                                                                                                                                                                                                                                                                                                                                               EP1033405-A2.
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                                                                                                                                                                 AAG60683;
    Matches
                                                                                                      RESULT 64
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99US-0139452P 99US-0139452P 99US-0139454P 99US-0139455P 99US-0139455P 99US-0139456P 99US-0139456P 99US-0139463P 99US-0139463P 99US-0139463P 99US-0139463P 99US-0139463P 99US-0139463P 99US-0139463P 99US-014055P 99US-014055P 99US-014299P 99US-014299P 99US-014298P 99US-014298P 99US-014298P 99US-014298P 99US-014298P 99US-014298P 99US-014298P 99US-014332P 99US-0144334P 99US-014488P 99US-014488P 99US-014488P 99US-014488P 99US-014488P 99US-014488P 99US-014488P 99US-014488P 99US-014488P 99US-014488P 99US-014488P 99US-014488P 99US-014488P 99US-014488P 99US-014488P	905 014508978978978978908 01451928908 014521489909 015 014521489909 015 014521489908 016 0145951989908 0145951989908 01470389908 014719289908 014719289908 014719289908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 014719328908 0147179328908 0147179328908 0147179328908 0147179328908 0147179328908 0147179328908 0147179328908 0147179328908 0147179328908 0147179328908 0147179328908 014717978908 014717978908 014717978908 014717978908 014717978908 01471799908 01471799908 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909 01471799909
16-40N-1999; 18 R R R R R R R R R R R R R R R R R R R	22 - UUL - 1999 23 - UUL - 1999 23 - UUL - 1999 23 - UUL - 1999 27 - UUL - 1999 27 - UUL - 1999 27 - UUL - 1999 02 - AUG - 1999 02 - AUG - 1999 03 - AUG - 1999 04 - AUG - 1999 05 - AUG - 1999 06 - AUG - 1999 06 - AUG - 1999 07 - AUG - 1999 08 - AUG - 1999 09 - AUG - 1999 09 - AUG - 1999 01 - AUG - 1999

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PR 13-AUC-1999) 99US-0144666P PR 16-AUC-1999) 99US-0144666P PR 16-AUC-1999) 99US-0144666P PR 16-AUC-1999) 99US-014466P PR 16-AUC-1999) 99US-0144672P PR 18-AUC-1999) 99US-014492P PR 18-AUC-1999) 99US-014492P PR 18-AUC-1999) 99US-014992P PR 18-AUC-1999) 99US-014993 99US-014993P PR 18-AUC-1999) 99US-014992P PR 18-AUC-1999) 99US-014992P PR 18-AUC-1999) 99US-014992P PR 18-AUC-1999) 99US-014993P PR 18-AUC-1999) 99US-014993P PR 18-AUC-1999) 99US-014992P PR 18-AUC-1999) 99US-014993P PR 18-AUC-1999) 99US-014
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Gaps

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AAM75737 standard; protein; 60 AA.
                                                                                                                                                                                                                                                                                                        Human genome-derived single exon agene expression in human placenta
                                                                                                              26-MAY-2000; 2000US-0207456P.
30-UIN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0235559P.
04-OCT-2000; 2000GB-00024263.
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2000US-00608408
2000US-00632366
2000US-0234687P
2000US-0236359P
2000GB-00024263
                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000668
                                                                  30-JAN-2001; 2001WO-US000663.
                                                                                                 2000US-0180312P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                               WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 VAEF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 60 AA;
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            WO200157272 - A2
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
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                                                                                                   04-FEB-2000;
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                                        09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and single exon nucleic acid probes derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #9883 encoded by probe for measuring placental gene expression.
                                                                                                                                             Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                 Peptide #9550 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 34679; 639pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosie;
genetic disorder.
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                             ABB42044 standard; peptide; 60 AA
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26-MX-2000; 2000US-0201456P.
30-UJN-2000; 2000US-00603408.
03-AUG-2000; 2000US-0053356.
21-SEP-2000; 2000US-023468TP.
04-GCT-2000; 2000US-0234559P.
                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                        04-FEB-2002 (first entry)
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483447/52
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                                                                                                                                                                                                           WO200157277-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                       09-AUG-2001
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                                                           ABB42044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
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   RESULT 65
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nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 4; Length 60; 100.0%; Pred. No. 8.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     claim 27; SEQ ID NO 36115; 654pp; English
Rank DR;
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43

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diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
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2000US-00608408.
2000US-00632366.
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2000US-0236359P.
2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                       4; Conservative
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                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                       8 VAEF 11
                                                                                                                                                                        2 VAEF 5
                                                                        Sequence 60 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157273-A2.
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21-SEP-2000; 2
27-SEP-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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Matches
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                                                                                                                                                                                     The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human brain expressed single exon probe encoded protein SEQ ID NO: 35030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                        Example 4; SEQ ID NO 36043; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                     h Similarity 100.0%; Score 19; DB 4; Length 60; Similarity 100.0%; Pred. No. 8.4e+02; 4; Conservative 0; Mismatches 0; Indels
                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR
                                                                                                                       gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM62925 standard; protein; 60 AA.
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30-JUN-2000; 2000US-0069408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023659P.
04-OCT-2000; 2000GB-00024263.
       (MOLE-) MOLECULAR DYNAMICS INC
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                                       Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                       Penn SG, Hanzel DK,
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                                                                        WPI; 2001-488900/53
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                            Sequence 60 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM62925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                    Gaps
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Length 60;
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95.0%; Score 19; DB 4; Length 60; 100.0%; Pred. No. 8.4e+02; ive 0; Mismatches 0; Indels
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WO200157182-A2
              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a human ORF polypeptide, a substrate for extracellular signal-regulated kinase, ERK-6. Substances that modulate the activity of the ORP polypeptide can be used to treat diseases selected from dermatemyositis, polymositis, inclusion body myositis, sarcoid myopathy, AZT myopathy, myocardial infarction, and ischaemia/reperfusion. The probes and antibodies can be used to detect the presence
                                                                                                                                                                                                                                                             ORF polypeptide; dermatomyositis; polymyositis; inclusion body myositis; sarcoid myopathy; AZT myopathy; myocardial infarction; ischaemia; ERK-6; extracellular signal-regulated kinase; reperfusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
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              Gaps
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.8.7e+02;
thes 0; Indels
100.0%; Pred. No. 8.4e+02; ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 100.0%; Pred. No. 8.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding ORF polypeptide.
                                                                                                                                                                                                                                      HLH domain of drosophila E-spl m5.
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                                                                                                                                                AAY17262 standard; peptide; 62 AA
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Best Local Similarity 100.
Matches 4; Conservative
 Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SUGE-) SUGEN INC.
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                                                                    VAEF 11
                                           2 VAEF 5
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17-JAN-2001; 2001WO-US001354
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2000US-0249214P.
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05-JAN-2001;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat discorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own production of (1). Additionally, (1)
polymucleotides may be used to produce the secreted (1), by inserting the
colling into a host cell and culturing the cell to express the
nucleic acids into a host cell and culturing the cell to express the
corrects and cancer metastases of haematopoietic-falated diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
cepresent sequences trom the present invention. AAK64942 to AAK84950 and AAM82169
represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Propionibacterium acnes polypeptides and polynucleotides encoding the
                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maisonneuve JL;
Jones R, Carter D;
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                                                                                                                                                                                     Claim 11; SEQ ID NO 18840; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 4; Length 62;
100.0%; Pred. No. 8.7e+02;
iive 0; Mismatches 0; Indels
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Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM65667 standard; protein; 62 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2002; 2002WO-US032727.
(HUMA-) HUMAN GENOME SCI INC.
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nes 4; Conservative
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                                     Barash SC,
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                                                                      WPI; 2001-483426/52.
N-PSDB; AAK64028.
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                                     Rosen CA,
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Matches
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polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
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Claim 7; SEQ ID NO 30343; 1481pp; English

The Invention Felaces to an isolated polymuclectice (ABM36524-ABM6436) and to accoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymuclectides (ABM36524-ABM6436) and to additionally encompases expression vectors and host cells comprising additionally encompases expression vectors and host cells comprising a polypeptide of the invention; an immune response specific for a P. acnes polypeptide of the invention; an ethod for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell spoulation comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polymptide and an isolated T cell spoulation comprising P. acnes polypeptides, untibodies, fusion proteins, T cell populations, or an express the polypeptides, and a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a protein; T cell populations or antigen-presenting cells that express the polymptides are useful for diagnosing, preventing or treating acnes polypeptides, polymorectides, antibodies, fusion protein. The polymuclectides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the primited search is useful for performing a diagnostic assay. The present sequence represents a specifically claimed P. acnes polypeptide which is the primited specification, but was this patent did not form part of the primited specification, but was obtained in electronic forms part of the primited specification, but was invention relates to an isolated polynucleotide (ACF64435-ACF64733) ftp.wipo.int/pub/published_pct_sequences

Sequence 62 AA;

Gaps ö 95.0%; Score 19; DB 6; Length 62; 100.0%; Pred. No. 8.7e+02; ive 0; Mismatches 0; Indels 4; Conservative Query Match Best Local Similarity Matches 4; Conserv

2 VAEF 5

VAEF 11

AAC09517 standard; protein; 64 AA

(first entry) 06-NOV-2001 AA009517;

Human polypeptide SEQ ID NO 23409.

Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis, tissue growth factor; immunomodulatory, cancer, leukaemia, nervous system disorders; arthritis; inflammation.

Homo sapiens.

WO200164835-A2.

07-SEP-2001.

26-FEB-2001; 2001WO-US004927

28-FEB-2000; 2000US-00515126 18-MAY-2000; 2000US-00577409

(HYSE-) HYSEQ INC

Tang YT, Liu C, Drmanac RT;

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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                           The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA0013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, itssue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                              Claim 20; SEQ ID NO 23409; 1399pp + Sequence Listing; English.
                         WPI; 2001-514838/56
                                                   N-PSDB; AAI89448
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Sequence 64 AA;

Gaps ö 95.0%; Score 19; DB 4; Length 64; 100.0%; Pred. No. 9e+02; ive 0; Mismatches 0; Indels Local Similarity 100. Query Match Matches

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ଟ 셤 RESULT 74

AAY48352 standard; protein; 67 AA AAY48352

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08-DEC-1999 (first entry) AAY48352;

Human prostate cancer-associated protein 49.

Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy; cancer; tissue specificity; human.

Homo sapiens

DE19811194-A1.

16-SEP-1999.

98DE-01011194.

10-MAR-1998;

98DE-01011194 10-MAR-1998;

(META-) METAGEN GES GENOMFORSCHUNG MBH.

Rosenthal ы́ Dahl Specht T, Hinzmann B, Schmitt A, Pilarsky C, WPI; 1999-519629/44. N-PSDB; AAZ33499.

agents.

New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic

Claim 22; 143; 194pp; German.

This invention describes novel nucleic acid sequences (A) that are expressed at high level in normal prostatic tissue. Polypeptides (I) encoded by (A) are used: (a) for identifying agents for treatment of

prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTS (expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTS. AAY48304-Y4456 represent peptides encoded by the expressed sequence tags described in the method the invention 

Sequence 67 AA;

ö Gaps ö 95.0%; Score 19; DB 2; Length 67; 100.0%; Pred. No. 9.4e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 4; Conservative

≿ ŏ RESULT 75

ABP31047 standard; protein; 68 AA.

08-JUL-2002 (first entry) ABP31047;

Human ORF20 protein, SEQ ID NO:40.

Human, ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibin; chemotactic; chemokinetic; fartility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nototropic; antipsoriatic; antidiabetic; cytostatic; nototropic; cardiant; hypotensive, antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.

WO200190366-A2.

29-NOV-2001.

24-MAY-2001; 2001WO-US017076.

24-MAY-2000; 2000US-0206690P

(CURA-) CURAGEN CORP.

Leach MD, Shimkets RA;

WPI; 2002-106200/14. N-PSDB; ABN75073. Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation.

Claim 10; Page 280; 2508pp; English.

Sequences ABB31028-ABB35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN7567 represent cDNAs encoding them. The invention also encompasses 

cc polypeptides at least 80% identical to the ORFI-ORF4534 (collectively cf. referred to as ORFX) proteins, polymucleotides at least 85% identical to the ORFX undered conditions of the combinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX proteins, antibodies and polymucleotides, the recombinant production of ORFX proteins, antibodies are polymucleotides of screening for modulators of ORFX proteins or activity, and methods of screening for modulators of ORFX proteins or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide crampe of biological activities, such as cytokine, cell proliferation, immune modulation, hadmatopolesis regulation, cell differentiation, immune modulation, hadmatopolesis regulation, cell differentiation, antiinflammatory activity, thrombolytic activity, named antiinflammatory activity, thrombolytic activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, other proliferative disorders such as sporlasis and benign tumours, other proliferative disorders such as sporlasis and benign tumours, or neurological disorders such as epolapsy and Alzheimer's disease, corter proliferative disorders such as sporlasis and benign tumours, or corpus transplantation, disorders of primers and infectious diseases caused by viral, bacterial, corrange disease, and infectious diseases caused by viral, bacterial, strangerials, in penetic diagnosis, in the detection of ORFX genomic sequences, in genetic diagnosis, and in frue specific and in forensic diseases which may be useful for studying the function and/or activity of ORFX protein, and in drug spreening of ORFX proteins may also be useful in the detection and cloning of homologous conditionally be useful for studying the function and or activity of ORFX protein, and in drug specific anticoders which are useful in the detection of ORFX protein, and in drug ö Query Match Best Local Similarity 100.... Best Local 4; Conservative Sequence 68 AA; 

Gaps ö 95.0%; Score 19; DB 5; Length 68; 100.0%; Pred. No. 9.6e+02; ive 0; Mismatches 0; Indels

່ເດ 2 VAEF ઠે g Search completed: May 24, 2004, 17:38:08 Job time : 53.7857 secs

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us-09-594-978a-3.rpr

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Cjaccesion: E64618
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.; Khalak, H.G.; Glodek, A.; Morkenn son, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Morkenn son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
Ajauthors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Tille: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: E64618
A;Accession: E64618
A;Molecule type: DNA
A;Residues: 1-48 «TOM»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown protein encoded within prophage CP-933R [imported] - Escherichia coli (strain C C,Species: Bacherichia coli (c)Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001 C,Accession: BS745 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayheviller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca A)Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A,Accesion: BS745 A88480; MUD:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE000591; GB:AE000511; NID:g2313918; PIDN:AAD07847.1; PID:g23139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physochetical protein (lon 5' region) - Bacillus brevis
C'Species: Bacillus brevis
C'Species: Bacillus brevis
C'Date: 10-741-1992 #sequence_revision 10-Jul-1992 #text_change 15-Oct-1999
C'Accession: A42375; 19873
R;Ito, K.; Udaka, 8.; Yamagata, H.
J. Bacteriol. 174, 2281-2287, 1992
A;Title: Cloning, characterization, and inactivation of the Bacillus brevis lon gene.
A;Reference number: A42375; MUID:92202157; PMID:1551846
                                                                                                                                                                                                                       hypothetical protein HP0789 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
Gaps
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95.0%; Score 19; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.46+02;
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Matches 4; Conserv
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C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Date: 09-Aug-1997 #sequence_revision, B.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Reference number: A64520; MUD:97394467; PMID:9252185
A;Accession: G64625
A;Accession: G64625
A;Accession: Jrellminary; nucleic acid sequence not shown; translation not shown
A;Accession: J.33 cTOM>
A;References: GB:AE000596; GB:AE000511; NID:92313982; FIDN:AAD07920.1; PID:9231400
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: 839049
R;Lutz, F:; Mohr, M.; Grimmig, M.; Leidolf, R.; Linder, D.
Bur. J. Biochem. 217, 1123-1128, 1993
A;Title: Fseudomonas aeruginosa cytotoxin-binding protein in rabbit erythrocyte membrane A;Reference number: 839049; MUID:94039134; PMID:7693466
A;Accession: S39049
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C,Superfamily: lens fiber membrane major intrinsic protein
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100.0%; Pred. No. 52;
tive 0; Mismatches 0
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T25551
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        B85045
Z2BPA4
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A10147
A91038
AF0808
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S31816
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G71308
A69312
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Best Local Similarity 100.
Matches 4; Conservative
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A;Molecule type: protein
A;Residues: 1-20 <LUT>
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A,Status: preliminary

conserved hypothetical protein AF1090 - Archaeoglobus fulgidus

Accession: A69386

95.0%; Score 19; DB 2; Length 54; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 4; Conservative

7;Genetics: 1;Gene: Z2382

32 VAEF 35

2 VAEF 5

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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Godzane, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J. Godzane, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; D.M.; Brandon, R.C.; Fine, L.D.; Pritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Status: nucleic acid sequence not shown; translation not shown A; Status: DNA A; Status: DNA A; Residues: 1-63 <-TIGRS A; Cross-references: GB:U32728; GB:L42023; NID:g1573425; PIDN:AAC22109.1; PID:g1573437; T
                                                                                                                                                                                                                                                  C.Accession: J. C.M. House, meducance_revision 14-Uul-1995 #text_change 20-Sep-1999
C.Accession: JG4002
R.Arisawa, A.; Tsunekawa, H.; Okamura, K.; Okamoto, R.
Biosci. Biotechnol. Blochem. 59, 582-588, 1995
A.Title: Nucleotide Sequence analysis of the Carbomycin biosynthetic genes including the A.Title: Nucleotide Sequence analysis of the Carbomycin biosynthetic genes including the A.Title: Nucleotide Sequence analysis of the Carbomycin biosynthetic genes including the A.Title: Nucleotide Sequence analysis of the Carbomycin biosynthetic genes including the A.Residues: 1-63 ARIS
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A.Residues: 1-63 ARIS
A.Cross-references: DDBJ:330759; NID:3551628; PIDN:BAA06419.1; PID:d1006989; PID:3551629
A.Note: the source was designated as Streptomyces thermotolerans
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A.Title: Characterization of the 5' region of the Atlantic salmon (Salmo salar) transfer
A.Reference number: 151350; MUID:95121925; PMID:7821802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homology
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C,Species: Salmo salar (Atlantic salmon)
C,Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein H10451 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: G64007
                                                                                                                                                                                                                       C;Species: Streptomyces sp.
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1999
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95.0%; Score 19; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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VAEF 15
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R; Kvingedal, A.M.
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Best Local S:
Matches 4
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Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: B71349
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-59 <COL>
A;Residues: 1-59 <COL>
A;Cross-references: GB;AE001205; GB:AE000520; NID:g3322501; PIDN:AAC65223.1; PID:g332250
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        % Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. sature 330, 3364-370, 1997.

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Wosse, C.R.; Venter, J.C.

Smith, H.O.; Wosse, C.R.; Venter, J.C.

A;Reference number: A69250; MUID:98049343; PMID:9389475
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C;Superfamily: Methanococcus jannaschii hypothetical protein MJ0975
       A.Molecule type: DNA
A.Residues: 1-54 <STO>
A.Residues: 1-54 <STO>
A.P.Cross-references: GB:AE005174; NID:g12515374; PIDN:AAG56425.1; GSPDB:GN00145; UWGP:Z23
A.Experimental source: strain O157:H7, substrain EDL933
J.Genetics:
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Archaeoglobus fulgidus
.Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jan-2000
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y Match 95.0%; Score 19; DB 2; Length 59; Local Similarity 100.0%; Pred. No. 1.6e+02; hes 4; Conservative 0; Mismatches 0; Indels

Query Match Best Loc Matches 51 VAEF 54

C; Accession: E71349

2 VAEF 5

à g 95.0%; Score 19; DB 2; Length 59; ilarity 100.0%; Pred. No. 1.6e+02; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 4; Conserv

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hypothetical protein BH2182 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: P83922
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir.
Nucleic Acids Res. 28, 4317-4331, 2000
A;Reference number: A33650; MUID:20512582; PMID:11058132
A;Accession: P83922
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C;Species: Chlorella virus PBCV-1
C;Species: Chorella virus PBCV-1
C;Accession: T18034
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ZC477.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0; Indels
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex
C;Accession: T27605
R;Du, Z.
submitted to the EMBL Data Library, November 1995
A;Bescription: The sequence of C. elegans cosmid ZC477.
A;Reference number: Z20392
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A;Molecule type: DNA
A;Residues: 1-79 <GRA>
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A,Molecule type: DNA
A,Residues: 1-79 <DUZ>
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Matches 4; Conservative
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Best Local Similarity
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A;Molecule type: DNA
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Gene: CBSP:ZC477.6
2 VAEF
                                                        VAEF
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C;Species: Clostridium acetobutylicum
C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: D97045
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
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C;Species: phage 186
C;Dates: 28-May-1993 #text_change 17-Mar-1999
C;Dates: 28-May-1993 #sequence_revision 28-May-1993 #text_change 17-Mar-1999
C;Accession: 807277; 825273
B;Kalionis, B.; Dodd, I.B.; Egan, J.B.
J. Mol. Biol. 191, 199-209, 1986
A;Titles: Control of gene expression in the P2-related template coliphages. III. DNA sequence number: 807277; MUID:87112711; PMID:3806670
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A; Readdues: 1-75 «XDL.)
A; Cross-references: EMBL:X04449; NID:915549; PID:915550
R; Dibbens, J.A.; Gregory, S.L.; Egan, J.B.
Mol. Microbiol. 6, 2642-2650, 1992
Mol. Microbiol. 6, 2642-2650, 1992
A; Title: Control of gene expression in the temperate coliphage 186. X. The cl repressor
A; Reference number: S25273; MUID:93078618; PMID:1447973
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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  A;Molecule type: DNA
A;Residues: 1-64 <KVI>
A;Croser references: GB:L26909; NID:g598395; PIDN:AAC42221.1; PID:g598396
C;Genetics:
A;Gene: Tf
A;Introns: 14/1
C;Superfamily: transferrin; transferrin repeat homology
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95.0%; Score 19; DB 2; Length 75;

Best Local Similarity 100.0%; Pred. No. 2.18+02;

Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                   Length 64;
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95.0%; Score 19; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-74 <KUR>
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A; Residues: 1-75 <DIB>
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A;Residues: 1-84 <STO>

C;Genetics: A;Gene: BH2182

38 VAEF 41

2 VAEF 5

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hypothetical protein Y1103 - Yersinia pestis plasmid pWT1
C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15018
R;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIMS plasmid
A;Reference number: Z18268; MUID:99043898; PMID:9826348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cjaccession: AB3053
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. R;Wood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell ; Karp, P.; Romero, P.; Zhang, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: F86618
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli debonem Ress. 11, 731-733, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactoccoccus lactis ss A;Reference number: A86625; WUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein ypjB (imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Atu4039 [imported] - Agrobacterium tumefaciens (strain C58,
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A,Experimental source: strain IL1403
C,Genetics:
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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                                                                             Indels
                                 Pred. No. 2.5e+02;
Mismatches 0;
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100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-89 <LIN>
100.08; FI.
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
                           Best Local Similarity
Matches 4; Conserv
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A, Molecule type: DNA
A, Residues: 1-89 <STO>
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"Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

"Species: 20-Sep191 #sequence_revision 20-Sep1991 #text_change 05-Dec-1997

"Ascession: A38725

"Tu, G.F.; Achen, M.G.; Aldred, A.R.; Southwell, B.R.; Schreiber, G.

"Tuich: Chem. 266, 6201-6208, 1991

"Airitle: The distribution of cerebral expression of the transferrin gene is species species companies of the c
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C;Superfamily: Escherichia coli ribosomal protein S15; eubacterial ribosomal protein S15
F;23-89/Domain: eubacterial ribosomal protein S15 homology <ES15>
                                                                                        4,Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05901.1; GSPDB:GN00
4,Experimental source: strain C-125
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C,Superfamily: transferrin; transferrin repeat homology
C,Keywords: duplication
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95.0%; Score 19; DB 2; L.
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0;
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4,Status: preliminary 4,Molecule type: mRNA 4,Residues: 1-87 <TUA>

13 VAEF 16

2 VAEF 5

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Molecule type: DNA Residues: 1-89 <TIG2>

Query Match

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RESULT 25
C64490
hypothetical protein MJI524 - Methanococcus jannaschii
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A:Molecule type: DNA
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Similarity 100.0%;
4; Conservative 0
A,Experimental source: strain PAO1
C,Genetics:
A,Gene: PA3202
                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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A;Gene: nifx
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C; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C; Date: 27-Nov-2001
R; Claser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mao, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: Ac1397
A; Status: preliminary
A; Molecule type: DNA
A; Status: DNA
A; DNA
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K.; Lim,
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A;Moleccule type: DNA
Residues: 1-99 <82TO>
A;Cross-references: GB:AE004744; GB:AE004091; NID:g9949317; PIDN:AAG06590.1; GSPDB:GNC01
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A.Accession: E83244
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C;Species: Pseudomonas aeruginosa
C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83244
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brady, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
   Science 294, 2317-2323, 2001
A,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                Ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Accession: AB3053

A;Status: preliminary

A;Nolecule type: DNA

A;Residues: 1-96 < KUR>

A;Cross-references: GB:AE008689; PIDN:AAL44840.1; PID:G17742484; GSFDB:GN00187

A;Experimental source: strain C58 (Dupont)
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A;Gene: Atu4039
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Conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Accession: H90297
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Accession: H90297
A;Accession: H90297
A;Accession: H90297
A;Molecule type: DNA
A;Molecule type: DNA
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J. Bacteriol. 179, 541-543, 1997
A; Hitle: Nitrogenase phylogeny and the molybdenum dependence of nitrogen fixation in Me
A;Reference number: Z16944; MUID:97144542; PMID:8990309
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A;Cross-references: GB:AE006641; NID:g13814625; PIDN:AAK41639.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO1404
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A;Cross-references: EMBL:U75887; NID:g1666882; PIDN:AAC45519.1; PID:g1666890
A;Experimental source: strain JJ
C;Genetics:
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T10097
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      Length 99;
95.0%; Score 19; DB 2; Le
ilarity 100.0%; Pred. No. 2.8e+02;
Conservative 0; Mismatches 0;
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Gaps

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us-09-594-978a-3.rpr

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bubmitted to the Brookhaven Protein Data Bank, June 1994
A;Reference number: A52519; PDB:1AKP
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
R;Zein, N; Casasza, A,M; Doyle, T.W; Leet, J.E.; Schroeder, D.R.; Solomon, W.; Nadler
Proc. Natl. Acad. Sci. U.S.A. 90, 8009/8012, 1993
A;Title: Selective proteolytic activity of the antitumor agent kedarcidin.
A;Reference number: A58601; MID:93376722; PMID:8367457
A;Contents: annotation; protein activity
C;Superfamily: macromomycin
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NyAlternate names: kedarcidin apoprotein
C;Species: Streptoalloteichus sp.
C;Species: Streptoalloteichus sp.
C;Species: Streptoalloteichus sp.
C;Avariety: strain L585-6 (ATCC 53650)
C;Date: 21-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 15-Sep-2000
C;Accession: A55872
C;Accession: A55872
J. Marson, J.A.; Malacko, A.R.; Marquardt, H.
J. Antibiot. 45, 1250-1254, 1992
A;Title: Kedarcidin, a new chromoprotein antitumor antibiotic. II. Isolation, purificati
A;Reference number: A55872; MUID:93015257; PMID:1399845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Alature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE004598; GB:AE004091; NID:g9947687; PIDN:AAG05111.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: pscI; PA1722
C;Superfamily: Yersinia enterocolitica plasmid pYV virC-region hypothetical protein yscI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type III export protein PacI PA1722 [imported] - Pseudomonas aeruginosa (strain PAOI) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83431
A;Experimental source: specific host Chlorella strain NC64
C;Genetics:
A;Gene: A92L
C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A92L
                                                                                                                                                                          95.0%; Score 19; DB 2; Length 111; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels
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95.0%; Score 19; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 4; Conservative
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Residues: 1-112 <STO>
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Advance 33, S37-544, 1998

A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference numbor: A70500; MUID:98295987; PMID:9634230

A; Status: Preliminary; nucleic acid sequence not shown; translation not shown

B; Resédiuse: Jane A
                                                                             Abult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Relative C.J.; White, O.; Olsen, G.J.; Zhou, L.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Science 273, 1058-1073, 1996
Aputhors: Kaine, P.W.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.J.; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.J.; Kreference number: A64300; MUID:96337999; PMID:8688087
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                          V;Status: preliminary; nucleic acid sequence not shown; translation not shown indecule type: DNA 1;Residues: 1-108 <BUL> <br/>V;Essidues: 1-108 <BUL> <br/>V;Cross-references: GB:U67593; GB:L77117; NID:g2826427; PIDN:AAB99550.1; PID:g1592154;
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Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
               Species: Methanococcus jannaschii
;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 12-Jun-2003
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A.Molecule type: DNA
A.Residues: 1-111 - GRANA
A.Cross-references: BMBL:U42580; NID:94028896; PIDN:AAC96460.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h Similarity 100.0%; Score 19; DB 2; Length 108; Similarity 100.0%; Pred. No. 3e+02; 4; Conservative 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Map position: FOR1501406-1501732
;Superfamily: uncharacterized conserved protein MJ1524
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R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T17582
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Best Local Similarity
Matches 4; Conserv
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C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: F9327
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow. R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilof A;Reference number: A95262; MUID:21396509; PMID:11481432
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A,Molecule type: DNA
A,Residuss: 1-119 <KUR>
A,Residuss: 1-119 <KUR>
A,Cross-references: GB.AE006469; PIDN:AAK65184.1; PID:g14523629; GSPDB:GN00165
A,Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
                   C;Accession: A01608
R;Hobart P.M.; Shen, L.P.; Crawford, R.; Pictet, R.L.; Rutter, W.J.
Science 210, 1360-1363, 1980
A;Title: Comparison of the nucleic acid sequence of anglerfish and mammalian insulin mR
A;Reference number: A94254; MUID:81056434; PMID:7001633
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: T48682
31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h Similarity 100.0%; Score 19; DB 2; Length 118; Similarity 100.0%; Pred. No. 3.3e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 116;
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95.0%; Score 19; DB 1; Length 116
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Note: DKFZp761N05121.1
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Best Local Similarity
Matches 4; Conserv
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A; Residues: 1-116 < HOB>
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A,Molecule type: mRNA
A,Residues: 1-118 <AAA>
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                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein AGR_C 804 [imported] - Agrobacterium tumefaciens (strain C58, Cered C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Accession: D97414
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, Cander Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: D7528
R,anonymous, Genoscope
submitted to the BMBL Data Library, July 1999
A;Reference number: A75001
A;Reference number: A75001
A;Reference number: A75001
A;Accession: D75218
A;Accession: D75218
A;Molecule type: DNA
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;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49195.1; PID:e151508
;Experimental source: strain Orsay
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Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
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                                                                                 Length 114;
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Pred. No. 3.2e+02;
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                                                                           Query Match 95.0%; Score 19; DB 2; L
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.2e+02
iive 0; Mismatches (
  C; Keywords: antibiotic; pigment binding F_137-47,88-95/Disulfide bonds: #status experimental
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C;Species: Lophius americanus (American goosefish)
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100.0%; Pred. No. ...
0; Mismatches
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100.0%; Fre
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conserv
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Molecule type: DNA
Residues: 1-114 <KUR>
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Query Match 95.0
Best Local Similarity 100.
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A;Molecule type: DNA
A;Residues: 1-126 <PAR>
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7; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent
3; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent
4; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
5; Reference number: A82515; MUID: 20365717; PMID: 10910347
7; Note: for a complete list of authors see reference number A59328 below
A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A;Residues: 1-122 <SIM>
A;Residues: 1-122 <SIM>
A;Cross-references: GB:AE003851, NID:g9112238; PIDN:AAF85575.1; GSPDB:GN00130; XFSC:XFad
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                                              L.; Hyman, R.W.; Jones, T.

Joience 293, 668-672, 2001

"Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

lebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.,

"Ittle: The composite genome of the legume symbiont Sinorhizobium meliloti.

"Reference number: A96039; MUID:21368234; PMID:11474104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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?,Species: Xylella fastidiosa
?,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
         Chain, P.; Cowie,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                    1; Gene: SMa0974
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C;Special MyCobacterium tuberculosis (strain H3/RV)
C;Specias: MyCobacterium tuberculosis
C;Specias: MyCobacterium tuberculosis
C;Date: 17-Unl-1998 #text_change 22-Oct-1999
C;Accession: D70790
R;Colo, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Parkhill, J.; Garnier, T.; Genles, S.; Hamlin, N.; Holroyd, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Genles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 193, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Accession: D70790
A;Cocsion: D70790
A;Accession: D70700
A;Acc
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C;Date: 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: B83368
K;Parkhil, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Reference number: A81250; MUID:20150912; PMID:10688204
ki, S.; Church, G.M.; Daniels, C.J.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A; Fitle: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Accession: B69129
A; Accession: B69129
A; Accession: D69129
A; Accession: Jerge: DNA
A; Residues: 1-125 < AFF
A; Residues: 1-125 < AFF
A; Residues: 1-125 < AFF
A; Residues: GB: AE000810; GB: AE000666; NID: G2621277; PIDN: AAB84740.1; PID: G262128
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A;Experimental source: serotype O2, strain NCTC 11168
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Pred. No. 3.5e+02;
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C, Superfamily: 4-carboxymuconolactone decarboxylase
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us-09-594-978a-3.rpr

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C,Accession: A54797
R;Crossman, M.W.; Hauft, S.M.; Gordon, J.I.
J. Cell Biol. 126, 1547-1564, 1994
A;Title: The mouse ileal lipid-binding protein gene: a model for studying axial pattern
A;Reference number: A54797; MUID:94375529; PMID:8089185
A;Accession: A54797
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C;Species: Thermotoga maritima
C;Species: 11.5un-1999 #sequence_revision 11.5un-1999 #text_change 21.5ul-2000
C;Accession: D72348
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A;Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable cathepsin B-like cysteine proteinase (EC 3.4.22.-) T15B16.17b - Arabidopsis th
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-19 < STO:
A; Cross-references: EMBL:AF104919; NID:93859590; PIDN:AAC72873.1; PID:93859607
A; Experimental source: cultivar Columbia
                                                                                                                         ileal lipid-binding protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Nov-1999
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.Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 22-Jun-1999
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A;Molecule type: mRNA
A;Readdues: 1-128 <CRO>
A;Cross-references: GB:U00938; NID:g507143; PIDN:AAC27352.1; PID:g507144
C;Genetics:
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3.6e+02;
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Local Similarity 100.0%; Pred. No. 3.7e+02;
Les 4; Conservative 0; Mismatches 0;
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R;Stoneking, T.; Smith, R.
submitted to the EMBL Data Library, November 1998
A;Description: The sequence of A. thaliana T15B16.
A;Reference number: Z14488
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A;Introns: 26/3; 44/3; 71/3
A;Note: 1131: papain
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
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C;Superfamily: myelin P2 protein
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.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: Ab1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Rv3747 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: D70799
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Naturner: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MuID:98295937; PMID:9634230
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A;Residues: 1-127 <GLA>
A;Crossreferences: GB:AL592022; PIDN:CAC97626.1; PID:g16414922; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AB1732
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                                                                                    Length 126;
                                                                                    95.0%; Score 19; DB 2; Le 100.0%; Pred. No. 3.6e+02; ive 0; Mismatches 0;
                                                                                    Query Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                    83 VAEF 86
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A, Gene: Cj0939c
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hypothetical protein alr1525 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. etrain PCC 7120
C;Accession: AG1996
N; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Shitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Yersinia peetis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AH0137
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia peetis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein YPO1120 [imported] - Yersinia pestis (strain CO92)
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A;Molecule type: DNA
A;Residues: 1-132 <UNA
A;Cross-references: GB:BA000019; PIDN:BAB77891.1; PID:g17135345; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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A;Residues: 1-133 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89963.1; PID:g15979187; GSPDB:GN00175
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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95.0%; Score 19; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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C;Superfamily: rbcX protein
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81 VAEF 84
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C,Species: Pyrococcus abyssi
C,Accession: G75208
R,anonymous, Genoscope
Submitted to the EMBL Bata Library, July 1999
A,Rescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struk, Accession: G75208
A,Rescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struk, Accession: G75208
A,Rescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struk, Reference number: A75001
A,Rocession: G75208
A,Residues: DAA
A,Residues: 1-131 < KGW>
A,Residues: 1-131 < KGW>
A,Residues: 1-131 cKGW>
A,Residues: Strain Orsay
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C;Species: Anabaena sp.
C;Species: Anabaena sp.
C;Species: Anabaena sp.
C;Species: Anabaena sp.
C;Accession: J02270
R;Larimer, F.W.; Soper, T.S.
Sene 126, 85-92, 1993
A;Title: Overproduction of Anabaena 7120 ribulose-bisphosphate carboxylase/oxygenase in A;Reference number: J02270; MUID:93231541; PMID:8472962
                                                                                                                     A;Cross-references: GB:AE001739; GB:AE000512; NID:g4981176; PIDN:AAD35739.1; PID:g498117
A;Experimental source: strain MSB8
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                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 2; Length 130; 100.0%; Pred. No. 3.7e+02;
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A;Gene: TM0655
C;Superfamily: conserved hypothetical protein MJ0315
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Best Local Similarity 100.0%; Pred. No. 3.7
Matches 4; Conservative 0; Mismatches
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Ryesidues: 1-132 CLAR>
A,Cross-references: DDBJ:U01540
A,Experimental source: strain 7120
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                             Status: preliminary
Molecule type: DNA
Residues: 1-130 <ARN>
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: C90725
R;Hayashi, T.; Maxino, K.; Ohnishi, M.; Xurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Hitle: Complete genome sequence of entexohemorrhagic Escherichia coli 0157:H7 and gen
A;Reference number: A99629; MUD:21156231; PMID:11258796
A;Accession: C90725
A;Accession: C90725
A;Acseluse: preliminary
A;Molecule type: DNA
A;Acseluse: 1-134 c4Ay>
A;Choserreferences: GB:BA000007; PIDN:BAB34194.1; PID:g13360230; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
G;Genetics: EC80771
C;Superfamily: 15.5K protein (tolAB operon 5' region)
hypothetical protein ybgC [imported] - Escherichia coli (strain 0157:H7, substrain EDL9 C;Species: Escherichia coli C;Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001 C;Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001 C;Datesion: BS576 E;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A88480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein EC80771 [imported] - Escherichia coli (strain 0157:H7, substrain F
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0. 3.8e+02; Indels
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95.0%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 3.8
Matches 4; Conservative 0; Mismatches
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A;Molecule type: DNA
A;Residues: 1-134 <STO>
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C.Species: Pab-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C.Accesion: A84221
R.MG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser: B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld
Jung, K.H.; Alam, M.; Frestas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Athors: Hud, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Sccession: A84221
A;Scatus: Preliminary
A;Molecule type: DNA
A;Scatus: Preliminary
A;Molecule type: DNA
A;Esidues: 1-133 <STO>
A;Cross-references: GB:AE004437; NID:g10580221; PIDN:AAG19133.1; GSPDB:GN00138
C;Genetics:
A;Gene: ribE
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C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Species: D-Our-1982 #sequence_revision 30-Jun-1988 #text_change 01-Mar-2002
C;Accession: A25880; G64809
R;Sun, T.P.; Webster, R.E.
J. Bacteriol. 169, 2667-2674, 1987
A;Title: Nuclectide sequence of a gene cluster involved in entry of E colicins and single Ascession: A25880,
A;Accession: A25880,
A;Accession: A25880
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A;Cross-references: GB:M16489; NID:g148021; PIDN:AAA83918.1; PID:g1128977
A;Cross-references: GB:M16489; NID:g148021; PIDN:AAA83918.1; PID:g1128977
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453.1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                A;Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12590.1; PID:g6460886; TIGR:DRE0d
A;Experimental source: strain R1
C;Genetics:
                                    A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: H75623
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A;Reference number: A64720; MUID:97426617; PMID:9278503
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Best Local Similarity 100.
Matches 4; Conservative
          Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                 A, Map position: megaplasmid
A, Genome: plasmid
A, Note: plasmid MP1
                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <WHI>
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Query Match

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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #text_change 03-Jun-2002
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: E8155
C;Accession: E8155
C;Accession: B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillir
C;W.; Ctail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyr
A;Accession: E8155
A;Accession: E8155
A;Accession: E8155
A;Accession: E8155
A;Residues: 1-137 <PAR>
A;Residues: 1-137 <PAR>
A;Residues: 1-137 <PAR>
A;Residues: 1-137 <PAR>
A;Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73094.1; PID:g696827
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribofjavin synthase beta subunit - Methanobacterium thermoautotrophicum (strain Delta H) C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-May-2000 C; Accession: A69062 R; Simith, D.R.; Doucette-Stamm, D.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Simith, D.R.; Doucette-Stamm, D.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H; funct A; Recession: A69062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Gross-references: GB:AE004292; GB:AE003852; NID:99656760; PIDN:AAF95344.1; GSPDB:GN001
A.Experimental source: serogroup 01; strain NI6961; biotype El Tor
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95.0%; Score 19; DB 2; L¢
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0;
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Docal Similarity 100.0%; Pred. No. 3.9e+02;
nes 4; Conservative 0; Mismatches 0;
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C, Superfamily: hypothetical protein yneT
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A,Map position: 1
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Matches
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%, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
NA Res. 3, 109-136, 1996
%; Yasuda Syana Syana Syana Syana Synechocystis
**Intle: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                      "Species: Salmonella enterica subsp. enterica serovar Typhi
'Species: Salmonella enterica subsp. enterica serovar Typhi
'Species: Salmonella enterica subsp. enterica serovar Typhi
'Note: this species has also been called Salmonella typhi
'Joace: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
'Accession: AD0592
'Accession: AD0592
'Accession: AD0592
'Accession: AD0592
'Accession: AD0592
'Accession: AD0592
'Adocora' P. 'Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
'S.; Moule, S.; O'Gaora, P.
'Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Atthors: Parry, C.; Quail, M.; Rutherford, M.; Simmonds, M.; Skelton, J.; Stevens, K.; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A'Cross-references: GB:AL513382; PIDN:CAD05206.1; PID:g16501976; GSPDB:GN00176
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is pecies Synechocystis sp.
is pecies Synechocystis sp.
is pecies 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
is pecies in S76416
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95.0%; Score 19; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                             Length 134;
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Similarity 100.0%; Pred. No. 3.8e+02;
4; Conservative 0; Mismatches 0;
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1,Status: preliminary
1,Molecule type: DNA
1,Residues: 1-136 <KAN>
                                                           Best Local Similarity
Matches 4; Conserv
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Gene: STY0790

≿ ă RESULT 55

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Genetics:

Query Match

ઠે a RESULT 58

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Fig. 15 Tribolatin synthase, subunit beta (ribE) homolog - Archaeoglobus fulgidus (Spacies: Archaeoglobus Habert, H.P.) Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodso (Spacies: Archaeomun, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 344-370, 1997 (Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A., Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woses, C. R.; Venter, J.C. A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeographic (Ph. 1995) (Ph. 199
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A; Cross-references: GB: AE000957; GB: AE000782; NID: G2689280; PIDN: AAB89124.1; PID: G26484
C; Superfamily: riboflavin synthase beta chain
                                                                                                                                               low-temperature regulated protein BN115 - rape
C;Species: Brassica napus (rape)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
C;Accession: JQ2279
R;Weretilnyk, B; Orr, W; White, T.C; Iu, B.; Singh, J.
Plant Physiol. 101, 171-77, 1993
A;Title: Characterization of three related low-temperature-regulated cDNAs from winter
A;Reference number: JQ2279; MUID:94105287; PMID:7904076
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C;Species: Brassica napus (rape)
C;Species: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
C;Accession: JQ2280
R;Meretilnyk, E; Orr, W.; White, T.C.; Iu, B.; Singh, J.
Plant Physiol. 101, 171-177, 1993
A;Title: Characterization of three related low-temperature-regulated cDNAs from winter
A;Reference number: JQ229; MUID:94105287; PMID:7904076
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A,Residues: 1-142 <WER>
A,Cross-references: GB:S68879; NID:g544695; PIDN:AAB29483.1; PID:g544696
C,Comment: This protein is a low-temperature-related protein.
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A;Residuses: 1-142 <WRS-
A;Cross-references: GB:S68726; NID:g544693; PIDN:AAB29482.1; PID:g544694
C;Comment: This protein is a low-temperature-related protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 2; Length 142;
100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
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Matches 4; Conservative 0
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
C;Accession: B69323
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUD:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A; Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-139 <GIS-
A,Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06320.1; GSPDB:GN00
A,Experimental source: strain C-125
        A;Cross-references: GB:AE000902; GB:AE000666; NID:g2622500; PIDN:AAB85867.1; PID:g26225d
A;Experimental source: strain Delta H
C;Genetics:
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C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF0586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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95.0%; Score 19; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     Similarity 100.0%; Score 19; DB 2; Length 139; Similarity 100.0%; Pred. No. 3.9e+02; 4; Conservative 0; Mismatches 0; Indels
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95.0%; Score 19; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                 A,Gene: MTH1390
C,Superfamily: riboflavin synthase beta chain
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A;Residues: 1-140 <KLE>
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Matches 4; Conserv
A;Residues: 1-139 <MTH>
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A;Gene: BH2601
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DNA Res. 3, 109-136, 1996
A,Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A Molecule type: DNA
A Residues: 1-147 <STO>
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Matanabe, A.; Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PI
                                                                                                                                                                                                                                                                                    orobable transposase, truncated section 1 [imported] - Streptomyces coelicolor (fragment); Species: Streptomyces coelicolor (fragment); Species: Streptomyces coelicolor (fragment); Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000; Accession: T36978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cibosomal protein L13 [similarity] - Haloarcula marismortui

S.Species: Haloarcula marismortui

S.Species: 11-011-2000 #sequence_revision 21-Jul-2000 #text_change 14-Apr-2003

S.Accession: B41715

S.Kroemer, W.J., Arndry, B.

S.Kroemer, W.J., Arndry, B.

Biol Chem. 266, 24573-24579, 1991

A,Title: Halobacterial S9 operon. Three ribosomal protein genes are cotranscribed with
                                                                                                                                                                                                                                                                                                                                                                                         %;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
1;Reference number: Z21618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ), Cross-references: EMBL:AL109949; PIDN:CAB52892.1; GSPDB:GN00070; SCOEDB:SCJ11.07c
A:Experimental source: strain A3(2)
D:Comment: A complete transposase sequence can be assembled from three adjacent orfs
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
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4;Residuss: 1-15 <KRO.
4;Crose-references: GB:M76567; NID:g148775; PIDN:AAA73097.1; PID:g148777
2;Guperfamily: ribosomal protein L13
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        Length 143
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95.0%; Score 19; DB 2; Length 143
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                       0; Indels
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4;Reference number: A41715; MUID:92105119; PMID:1840597
4;Accession: B41715
     DB 2; Le
. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V.Status: preliminary, translated from GB/EMBL/DDBJ/Molecule type: DNA
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  Query Match 95.0%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 4.1 Matches 4; Conservative 0; Mismatches
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100.0%; Pred. No.
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Best Local Similarity
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hypothetical protein Vng1398c [imported] - Halobacterium sp. NRC-1
CiSpecies: Halobacterium sp. NRC-1
CiSpecies: Halobacterium sp. NRC-1
CiSpecies: G2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
CiAccession: CG4294
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, E.
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Jasky, E.
Jung, K.H.; Alam, M.; Freitas, T.
Proc., Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Dannists, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: Only Apply 1000 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
Cispecies 1011 F89837
Rivaroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R; Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A; Title: Mole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; MUID:21311952; PMID:11418146
                                         A;Accession: S77043
A;Status: nucleid acid sequence not shown; translation not shown
A;Status: nucleid acid sequence not shown; translation not shown
A;Rosidues: 1-145 «KAN»
A;Rosidues: 1-145 «KAN»
A;Cross-references: EMBL:D64005; GB:AB001339; NID:g1001779; PIDN:BAA10735.1; PID:g10065:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein s110678
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A;Experimental source: strain N315
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Similarity 100.0%; Pred. No. 4.1e+02;
4; Conservative 0; Mismatches 0; Indels
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A; Reference number: S74322; MUID: 97061201; PMID: 8905231
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Riglaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, F. D.; Jones, L.M.; Karek, U.
D.; Jones, L.M.; Karek, U.
Science 294, 849-852, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; N.
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A; Feference number: AB1077; MUID:21537279; PMID:11679669
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C;Species: Agrobacterium tumefaciens
C;Species: 11.-dan-2002 #sequence_revision 11.-dan-2002 #text_change 18-Nov-2002
C;Accession: AB2857
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel * Karp, P.; Romero P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5-phosphate isomerase homolog lmo0498 [imported] - Listeria monocytogenes (strai
R;Zwickl, P.; Fabry, S.; Bogedain, C.; Haas, A.; Hensel, R.
J. Bacteriol. 172, 4329-4338, 1990
A;Title: Glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaebact
scherichia coli.
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Ajtile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
Ajritle: The Genome of the NulD:21608550; PMID:11743193
Ajacession: AB2857
Ajacession: AB2857
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A;Molecule type: DNA
A;Residues: 1-149 <GLA>
A;Residues: 1-149 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC98577.1; PID:g16409874; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AC1137
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Modecule type: DNA
A,Residues: 1-148 < ZWI>
A,Note: the authors translated the codon GGT for residue 54 as Glu
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Local Similarity 100.0%; Pred. No. 4.2e+02;
nes 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                A; Reference number: $10650; MUID:90330536; PMID:2165475
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100.0%; Pred. No. 4.2e+02;
tive 0; Mismatches 0;
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CiAccession: 734803
RiMurphy, Li, Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, June 1998
A, Accession: 734803
A, Stetus: preliminary; translated from GB/EMBL/DDBJ
A, Stetus: preliminary; translated from GB/EMBL/DDBJ
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CiDate: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993
CiAccession: S10655
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95.0%; Score 19; DB 2; Length 147;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                              0; Indels
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                      Query Match
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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S10655
hypothetical protein X - Pyrococcus woesei (fragment)
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Gene: NMA2160

, Gene: Atu2283

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Search completed: May 24, 2004, 17:38:38 Job time : 13.5 secs
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3;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Malx, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Affiche Comparative genomics of Listeria species.

4;Affiche Comparative genomics of Listeria species.

5;Accession: A1152
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Science 
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;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
;Accession: AB1089
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Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Accession: Al1452
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                                                                                                                95.0%; Score 19; DB 2; Length 150; 100.0%; Pred. No. 4.3e+02; tive 0; Mismatches 0; Indels
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.;Map position: circular chromosome ;Superfamily: plastocyanin
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yMolecule type: DNA
yResidues: 1-150 <GLA>
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87263
C;Accession: H87263
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon H. J.; Ermolaeva, M.; White, O.; Salzaberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. US.A. 99, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-151 <STO>
A;Cross-references: GB:AE005673; NID:g13421228; PIDN:AAK22108.1; GSFDB:GN00148
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Matches 4; Conservative
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GenCore version 5.1 Copyright (c) 1993 - 2004 Com	OM protein - protein search, using sw model Run on: May 24, 2004, 17:33:28 ; Search (with	<pre>litle: US-09-594-978A-3 Parfect score: 20 Sequence: 1 XVAEF 5</pre>	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	hed: 141681 seqs, 52070155 r	Total number of hits satisfying chosen parameters Minimum DB seq length: 0 Maximum DB seq length: 2000000000	ocessing	Database : SwissProt_42:*	Pred. No. is the number of results predict score greater than or equal to the score cand is derived by analysis of the total sc	SUMMARIES	* Result Query No. Score Match Length DB ID	19 95.0 19 1	23 23 23 23 23 23 23 23 24 24 24 24 24 24 24 24 24 24 24 24 24	19 95.0 88 1 19 95.0 93 1	19 95.0 108 1 19 95.0 114 1	19 95.0 115 1 19 95.0 116 1	19 95.0 119 1	19 95.0 122 1	19 95.0 127 1	19 95.0 130 1 19 95.0 131 1	19 95.0 133 1	19 95.0 139 1	19 95.0 140 1 19 95.0 143 1	19 95.0 145 1	19 95.0 1489 1	19 95.0 150 1 19 95.0 152 1	19 95.0 154 1 19 95.0 155 1	19 95.0 157 1 19 95.0 157 1	19 95.0 163 1 19 95.0 166 1

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Column	P52481 rattus norv P52481 rattus norv P26404 salmonella Q09357 caenorhabdi	P71528 methanococc P58394 rhizobium m	Q92vm6 rhizoblum m Q8g5f3 bifidobacte	Ognon3 ovis aries				013425 candida alb	P13925 streptococc	P44715 h pts syste	O59602 neisseria g	OBG6KU biridobacte O98481 rhizobium l	Q9jvq5 neisseria m	O9kono neisseria m	P1261/ anser anser P41843 caenorhabdi	067775 a bifunctio	048956 sorghum bic	P38776 saccharomyc	P19571 bacillus sp	Q9zge8 heliobacill	P09788 pseudomonas	P12336 rattus norv	P44706 haemophilus	P14246 mus muscuiu P11168 homo sapien	014344 schizosacch	Q8y275 ralsconia s 014498 homo sapien	OBVh51 mus musculu	Q28811 potorous tr	P41636 pinus taeda	Q8ubm8 a bifunctio	QByj53 b bitunctio 012899 homo sapien	Q7yr34 pan troglod	QBns31 corynebacte 007899 vibrio chol	O15891 tetrahymena	Objtwi neisseria m Objtwi neisseria m	Q9wz56 thermotoga	Oscniz pasteurella	P41988 caenorhabdi	Q9kuy4 vibrio chol	Q21802 caenornabdı ORdaya vibrio vuln	P09434 rhodobacter	Q8ctn9 staphylococ	Ogye64 aeropyrum p	lactobacil	P31883 WOllnella s O9z4i3 treponema m		Ogzmj6 helicobacte Ogwyke streptococo	56124	Q9j5h9 fowlpox vir P40720 salmonella
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085064 buchnera ap 007109 enterococcu 093744 pyrococcus Q10512 mycobacteri Q7w2y3 bordetella Q7w2y3 bordetella Q7w2y3 bordetella P48293 spirulina p P41563 bos taurus P50213 homo sapien P44502 haemophilus	P48288 corynebacte Q64913 african hor Q64313 african hor Q64354 clostridium Q58694 methancocc P15263 bacillus st P42442 corynebacte P16689 escherichlia Q9ras9 lactococcus Q9ckb7 pasteurella P36981 neurospora Q8fpd3 corynebacte P41391 schizosacch P45513 citrobacte P45513 citrobacter Q8rhd0 fusobacter Q8rhd0 fusobacter Q8rhd0 fusobacteri P55626 rhizobium s	P131373 acccharomyc P16622 saccharomyc O67781 aquifex aeo O51801 pyrococcus O58413 pyrococcus O58421 pyrococcus O58421 pyrococcus O67213 aquifex aeo O57213 aquifex aeo O58215 bacteroides O58225 amethanococc O8415 amethanococc O8415 aeoherichia O13883 schizobacteri O58596 archaeoglob O35594 mis musculu	P20828 drosophila P20828 drosophila P22993 alcaligenes O85718 acinetobact D40038 saccharomyc Q24338 drosophila Q26458 drosophila Q26458 drosophila Q26458 drosophila P4687 salmonella P22937 secherichia P22937 secherichia P40973 lilium long Q3pror ureaplasma P3584 candida alb P3584 bacillus su Q07478 saccharomyc Q83985 rieponema P P57351 buchnera ap Q98166 lacanobia o Q58947 rana catesb Q57918 mechanococc P37197 escherichia P51464 rana catesb Q57918 mechanococc Q95938 riekettsia aln
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P26334 trypanosoma
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Prasad H.K., Annapurna P.S.;
Submitted (DEC-1997) to Swiss-Prot.
Submitted (DEC-1997) to Swiss-Prot.
-!- SIMILARITY: STRONG, TO THE N-TERMINALS OF C.ELEGANS F20A1.4
AND H.INFLUENZAE H10967.
-!- CAUTION: We are unable to find this protein in the translation of the geneme of strain H37Rv.
NON TER 19 19
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083263;
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Preprotein translocase secE subunit.
SECE OR TP0235.
Treponema pallidum.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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MEDLINE=98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
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P22351
P57631
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asteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
(CEI_TaxID=1773;
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19 AA; 2211 MW; ABC1854BFIFFIF70 CRC64;
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15-771-1999 (Rel. 38, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
30 kDa non-secretory protein 2 (Fragment).
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11 VAEF 14
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P81136;
     SEQUENCE
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MEDLINE=98049343, PubMed=9389475,
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MEDLINE=98049343, PubMed=9389475,
MEDLINE=98049343, PubMed=9389475,
MEDLINE=98049343, PubMed=9389475,
MELON D. (Layton R.A., Tomb J.-F., White O., Nelson K.E.,
Metchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richaess E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Mixhess E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Pujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                spirochete.";
Science 281:375-388(1998).
-1- FUNCTION: 355-388 (1998).
-1- SUBCELLULAR LOCATION: Tail-anchored membrane protein (Potential).
-1- SIMILARITY: Belongs to the secE/SEC61-gamma family.
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InterPro; IPR001901; SecE.
PricerPro; IPR0050907; SecE. bac.
TIGRFAMS; TIGR00964; 3a0501806; 1.
PR051TE; P801067; SECE SEC61G; 1.
PR051TE; P801067; SECE SEC61G; 1.
TRANSMEM 39 59 POTENTIAL.
SEQUENCE 59 AA; 6789 Wm. COUNTIAL.
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren B., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T. McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.
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Nature 390:364-370(1997).
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Archaeoglobaceae, Archaeoglobus.
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100.0%; Pred. No. 1.1e+02;
iive 0; Mismatches 0;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical UPF0165 protein AF1090.
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YA90 ARCFU

AC 029175;
AD 16-OCT-2001
DT 16-OCT-2001
DT 15-OCT-2001
DE HYPOTHETICAL
GN ARCHAGAS, BUT
OC Archagas, BUT
CO Archagas, BUT
RA RIBURLING-9804
RA KIENK H.-P.
RA KIGHARGEN I
RA KICKNESS E.)
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Length 63;

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Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                              27 VAEF 30
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                                                                          2 VAEF 5
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                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMED outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RICINE-95350630, PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hechlow E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 1; Length 59; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                 InterPro; IPR008203; DUF104.
InterPro; IPR008204; DUF104_N.
Pfam; PF01954; DUF104; 1.
ProDom, PD005964; DUF04_N; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 59 AA; 6887 MW; B72E847382B2B6B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein, Complete proteome.
SEQUENCE 63 AA, 7047 MW, 36B14E60AC306B67 CRC64;
-!- SIMILARITY: Belongs to the UPF0165 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
48-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein H10451.
                                                                                                                                                                                           EMBL; AE001028; AAB90157.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32728; AAC22109.1; -. PIR; G64007; G64007.
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                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
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                                                                                                                                                                                                               PIR; A69386; A69386.
TIGR; AF1090; -
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:51_HAEIN
) _Y451_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAINSEA( / KW20 
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-I-FUNCTION: This procein is one of the 16S ribosomal RNA binding proceins (By similarity).
-I-SIMILARITY: Belongs to the S15P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update)
28-REB-2003 (Rel. 41, Last annotation update)
30S ribosomal protein S15.
(RPSO-A OR RPSIS-A OR HI1328) AND (RPSO-B OR RPSIS-B OR HI1468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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Pasteurellaceae, Haemophilus.
NCBI_TaxID=727,
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Ribosomal protein; rRNA-binding; Complete proteome.
INIT MET 0 0 0 BY SIMILARITY.
95.0%; Score 19; DB 1; Lv
100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0;
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InterPro; IPR005290; Ribosomal S15.b.
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ProDon, PD157043, RS15 bact, 1.
TIRFANS, TIGR00952, S15 bact, 1.
PROSITE, PS00362, RIBOSOMAL_S15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RS15 HAEIN STANDARD;
P44389;
01-NOV-1995 (Rel. 32, Created)
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                                                                                                           4; Conservative
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HSSP; P05766; 1A32.
TIGR; H11328; -
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Best Local Similarity
Matches 4; Conserv
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Methanococcus jannaschii
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KEDA ACTSL
ID KEDA ACTSL
AC P41249;
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                                                                                                                       North-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
ANA-binding protein Alba 2.
Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 93; 100.0%; Pred. No. 1.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Probon; PD010497; DUF78; 1.
TIGREAMS; TIGR00285; 1.
DIA-binding; Acetylation; Complete proteome.
MOD RES
SEQUENCE 93 AA; 10142 MW; E11D650FD5F63169 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AA
                               93 AA
                                                                                                                                                                                                                                                                                                                                                          EMBL; AE010398; AAM02302.1; -.
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16-0CT-2001 (Rel. 40, Last st
16-0CT-2001 (Rel. 40, Last at
Hypothetical protein MJ1524.
                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_01122; -; 1.
InterPro; IPR002775; DUF78.
Pfam; PF01918; DUF78; 1.
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Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 VAEF 50
                                                                                                            NCBI_TaxID=2320;
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                                                                                                   Methanopyrus
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(D_YF24_METJA
\C_Q589<u>1</u>9;
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                                                                                                                                    SECURNCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=5633999; PubMed=8680807;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Rolodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
Jannaschii.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 53650 / L585-6;

MEDLINE=93015257; PubMed=1399845;

Hoferead S.J., Matson J.A., Malacko A.R., Marquardt H.;

"Kedarcidin, a new ohromoprotein antitumor antibiotic. II. Isolation,

purification and physico-chemical properties.";

J. Antibiot. 45:1250-1254(1992).
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MEDLINE=93376732; PubMed=8367457;
Zein N., Casazza A.M., Doyle T.W., Leet J.E., Scheoeder D.R.,
Solomon W., Nadler S.G.;
Solomon W., Nadler S.G.;
Selective proteolytic activity of the antitumor agent kedarcidin.";
Proc. Natl. Acad. Sci. U.S.A. 90:8009-8012(1993).
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 1; Length 108; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
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InterPro; IPR003793; DUF190,
InterPro; IPR003793; DUF190,
Pfam; PF02641; DUF190; 1.
Hypothetical protein; Complete proteome.
REQUENCE 108 AA; 12398 MW; D3E286AFB9D4AF8B CRC64;
Archaea; Euryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE UPF0166 FAMILY.
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U67593; AAB99550.1; -. PIR; C64490; C64490.
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4; Conservative
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SEQUENCE OF 25-54 AND 96-116.
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DISULFID
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   STRAIN-ATCC 53650 / L585-6;

MEDLINE-95001848; PubMed=7918358;

CONSTANTANCE 53650 / L585-6;

MEDLINE-95001848; PubMed=7918358;

CONSTANTANCE 5... Colson K.L., Wittekind M., Friedrichs M.S.,

Zein N., Tuttle J., Langley D.R., Leet J.E., Schroeder D.R., Lam K.S.,

Farmer B.T. II, Metzler W.J., Bruccoleri R.E., Mueller L.;

Sequential IH, 13-7, and 15N NMR assignments and solution

conformation of apokedarcidin. "Sequential IH, 13-11452 (1994).

FINATION: BINDS NOW-COVALENTY TO AN ENEDITYE CHROMOPHORE WHICH IS

THE CYTOTOXIC AND WUTAGENIC COMPONENT OF THE ANTIBIOTIC. THE

CHROMOPHORE CLEAVES DUPLEX DNA SITE-SPECIFICALLY IN A SINGLE-
STRANDED MANNER. THE APOPROTERY CLEAVES PROTEINS BEING CLEAVED

THE MORE READILY.

THE MORE READILY.

STRANDED ANTIPERALLEL BETA-BARREL DOMAIN LINKED TO A SUBDOMAIN

COMPOSED OF TWO BETA-HARREIN RIBBONS.

STRANDED ANTIPERALLEL BETA-BARREL DOMAIN LINKED TO A SUBDOMAIN

COMPOSED OF TWO BETA-HARREIN RIBBONS.
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Verasper.

NCBI_TAXID=98923;
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the neocarz PDB; 1AKP; 31-AUG-94.
InterPro; IPR002186; Neocarzinostat.
Pfam; PF00960; Neocarzinostat. 1.
Probom; PD012709; Neocarzinostat. 1.
Antibiotic; DNA-binding; 3D-structure.
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ses 4; Conservative
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                                                                                                                                                                                                                                                                                                                                     112
114 AA;
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Andoh T., Nagasawa H.;
"Two molecular forms of insulin from barfin flounder, Verasper moseri, are derived from a single gene.";
are derived from a single gene.";
2001. Sci. 15:931-937(1998)
-!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synchesis in liver.
-!- SUBGNIT: Heterodimer of a B chain and an A chain linked by two
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MEDLINE=81056434; PubMed=7001633;
Hobbart P.M., Shen L.-P., Crawford R., Pictet R.L., Rutter W.J.;
"Comparison of the nucleic acid sequence of anglerfish and mammalian insulin mRNA's from cloned CDNA's.";
Science 210:1360-1363(1980).
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Bukaryota, Metazoa, Chordate, Craniata, Vertebrates, Euteleostom;
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha; Paracanthopterygii, Lophiiformes; Lophiidae; Lophius.
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INSULIN A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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100.0%; Pred. No. 2e+02;
:ive 0; Mismatches 0; Indels
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HSSP; PO1315; IMPJ.
PRO04925; Insylin; 1.
PRINTS; PRO0409; Insylin; 1.
PRINTS; PRO077; INSULINB.
SMART; SMO078; INSULINB.
SMART; SMO078; INSULINB.
INSULIN FOSOE22; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                         disulfide bonds.
-!- SUBCELLUTAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the insulin family.
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INSULIN B CHAIN.
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56
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115 AA;
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Best Local Similarity
Matches 4; Conserv
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PRT;
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062786;
28-FEB-2003 (Rel. 41, Created)
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InterPro, IPR007967; DUF727.
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GTR2_PIG
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                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the insulin family.

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                                                                                 Hoppe-Seyler's Z. Physiol. Chem. 350:1286-1288(1969).

-!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.

-!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewiss S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Bradopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
SPECIES=L.piscatorius;
MEDLINE=70036220; PubMed=5389298;
Neumann P.A., Koldenhof M., Humbel R.E.;
"Amino acid sequence of insulin from the angler fish (Lophius
piscatorius).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 116; 100.0%; Pred. No. 2.16+02; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, PO1308; 1LPH.
InterPro; IPR004825; Ins/IGF/relax.
Pfam; PF00499; Insulin; 1.
SMART; SM00078; INSULINB.
PROSITE; PS00262; INSULINB.
INSULINB; PS00262; INSULIN; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal.
SIGNAL
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UPF0279 protein CG14505.
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INSULIN A CHAIN.
INTERCHAIN.
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PIR; A01608; IPAF.
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STRAIN=Berkeley;
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RESULT 11 U279_DROME

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RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Rallawin D., Ra Ballew R.M., Basua A., Barendale U., Bayeraktaroglu L., Basaley E.M., Besson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.R., Besson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.R., Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I., Rherry J.M., Cawley S. Dahler C., Davenport L.B., Davies P., Dorbor B. Dahlos B., Deldher A., Deng Z., Mays A.D., Deng I., Durbin K.J., Evangelista C.C., Perraz C., Perraca S., Pleischmann W., RA Dodson K., Doup L.B., Gaven M.S., Gelbart W.M., Glasser K., A Dodson K., Doup L.B., Garg N.S., Gelbart W.M., Glasser K., A Goldo F., Gornell J.H., Gu Z., Kennison D., Houck J., Harvey D.A., Heiman T.J., Wal M.-H., Ibegwam C., Ratris N.L., Harvey D.A., Heiman T.J., Wal M.-H., Ibegwam C., Ratris N.L., Harvey D.A., Heiman T.J., Wal M.-H., Ibegwam C., Lei Y., Evalus F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lasko P., Lei Y., Leiltrisk A.A., Liu X., Mattei B., McIntosh T.C., McLeod M.P., Morberson D., Lasko P., Lei Y., McIntosh T.C., Morisd J., Morberson D., Lasko P., Morberson D., Lasko P., Morberson D., Lasko P., Nolson K., Nucholy M., Murphy B., Murphy L., Murry D.M., Nelson D.K., Nalson K.A., Nixon K., Nuchoed M.P., Panti V., Reese M.G., Rallanders R., Sprafling A.C., Staplecton M., Strong R., Sun E., Sprafling A.C., Staplecton M., Strong R., Sun E., Sprafling A.C., Staplecton M., Strong R., Sun E., Ray G., Lastor P., Walliams S.M., Woodage T., Worley K.C., Mang S., Pan S., Zho S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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MEDLINE=2246606; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Calniker S.B.;
"A Drosophila full-length CDNA resource.";
Genome Biol 3:RESEARCH0080.1-RESEARCH0080.8(2002).
-: SIMILARITY: Belongs to the UPF0279 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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SEQUENCE 119 AA; 13534 MW; 83FA23FCCCE389AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Le
100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0;
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Pyrobaculum aerophilum.

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           SOCOCOCOCOCETTARRESTER
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                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Canty J.M., Young R.F., Fallavollita J.A.;

In Facilitative glucose transporter. This isoform likely mediates the bidirectional transfer of glucose across the plasma mediates the bidirectional transfer of glucose membrane of hepatocytes and is responsible for uptake of glucose by the beta cells, may comprise part of the glucose-sensing mechanism of the beta cell. May also participate with the Na(+)/glucose cotransporter in the transcellular transport of glucose in the small intestine and kidney (By similarity).

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: Belongs to the sugar transporter family. Glucose transporter subfamily.
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-Oute carrier family 2, facilitated glucose transporter, member 2 (Glucose transporter type 2, liver) (Fragment).
SLC2A2 OR GLUT2.
                                                                                                                       Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartlodactyla; Suina; Suidae; Sus.
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InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sub_transporter.
InterPro; IPR005829; Sugar_transpt.
Pfor083; Sugar_tri, 1.
PRINTS; PR00171; SUGRTRNSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT 1; FARTIAL.
PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
Transmembrane; Sugar_transport; Transport; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 1; Length 120;
100.0%; Pred. No. 2.18+02;
ive 0; Mismatches 0; Indels
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13503 MW; DSF73168DBF03203 CRC64;
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CYTOPLASMIC (POTENTIAL).
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18E_PYRAB
D_R18E_PYRAE STANDARD; PRT; 122 AA.
T_28-FEB-2003 (Rel. 41, Created)
T_28-FEB-2003 (Rel. 41, Last sequence update)
T_28-FEB-2003 (Rel. 41, Last annotation update)
E_50S_tibosomal protein L18e.
N_RPL18E_OR_PAE0672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF054835; AAC12737.1; -.
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Best Local Similarity 100.
Matches 4; Conservative
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57
78
85
106
120
120 AA;
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                                                                                                                                                                                                   Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                SEQUENCE FROM N.A.
STRALM=INZ / ARTC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 1; Length 122
100.0%; Pred. No. 2.2e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSOI106; RIBOSOWAL LIBE; FALSE NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 122 AA; 13252 MW; 88F3DB732C4E0394 CRC64;
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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PIRSF; PIRSF000029; Cytochrome_b562; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein PM0670 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF 00329; -; 1.
InterPro; IPR001199; Ribosomal_L15.
InterPro; IPR000039; Ribosomal_L18e.
Ffam; PF00256; L15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE009779; AAL62941.1; -. HAMAP; MF_00329; -; 1.
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Best Local Similarity luv...
Sest Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                        NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 VAEF 38
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                                                                                                                                                                                                                                 aerophilum.";
                                                                                                                                                                                       Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Pm70
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Y670 PASMU
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NCBI_TaxID=2336;
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                             SPEH THEMA
Q9WZC3;
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                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crossman M.W., Hauft S.M., Gordon J.I.;
"The mouse ileal lipid-binding protein gene: a model for studying axial patterning during gut morphogenesis.";
J. Gell Biol. 126:1477-1564(1994).
-:- FUNCTION: ILEAL PROTEIN WHICH STIMULATES GASTRIC ACID AND PEPSINOGEN SECRETION. SEEMS TO BE ABLE TO BIND TO BILE SALTS AND
                                                                                                                                                                                                                                                                                                                                                                         PABPE OR ILLBP.

Was musculus (Mouse).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BILIRUBINS. SUBCELLULAR LOCATION: Cytoplasmic. SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: Belongs to the fatty-acid binding protein (FABP)
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                                                                              Score 19; DB 1; Length 124;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prime, PR00178; ca...; Pressive Property Property PR051TE; PS00214; FABP; 1.
Transport; Lipid-binding; Acetylation.
Transport; Lipid-binding; Acetylation.
Transport; Lipid-binding; Description (BY SIMILARITY).
1 1 ACETYLATION (BY SIMILARITY).
1 1 ACETYLATION (BY SIMILARITY).
Hypothetical protein; Signal; Complete proteome.
SIGNAL 1 24 PROTENTIAL.
CHAIN 24 HYPOTHETICAL PROTEIN PM0670.
SEQUENCE 124 AA; 13746 MW; D7B2B4885C7B51B9A CRC64;
                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                        01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
10-0cT-2033 (Rel. 42, Last annotation update)
Gastrotropin (GT) (Ileal lipid-binding protein) (ILBP).
                                                                     95.0%; Scor.
100.0%; Pred. No. ...
'... 0; Mismatches
                                                                                                                                                                                                                                                                        127 AA
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InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; iipocin_cytFABP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-DBA/2J; TISSUE-Liver;
MEDLINE-94375529; PubMed-8089185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000566; Lipocln_c
Pfam; PF00061; lipocalin; 1.
PRINTS; PR00178; FATTYACIDBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U00938; AAC27352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A54797; A54797.
                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                    45 VAEF 48
                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                     ILBP MOUSE
P51162;
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VAEF 94

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SEQUENCE FROM N.A.

SEQUENCE PROM N.A.

MEDIAN 3.09 / ATCC 43589;

MEDIAN 3.09 / ATCC 43589;

MEDIAN 3.00 / ATCC 43589;

MEDIAN 3.00 / ATCC 43589;

MEDIAN 4. Hickey E.K., Deterson J.D., Melson W.C., Ketchum K.A.,

A Release A.M., Cotton M.D., Pratt M.S., Dillips C.A., Richardson D.,

A Hidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,

Salzberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,

A Salzberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,

A Salzberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,

A Salzberg J., Sutton G.S., Pleischmann R.D., Eisen J.A., White O.,

A Salzberg J., Sutton G.S., Pleischmann R.D., Eisen J.A., White O.,

A Salzberg J., Sutton G.S., Pleischmann R.D., Eisen J.A., White O.,

Benome sequence of Thermotoga maritima.";

Nature 339:323-329(1999).

-I FUNCTION: Decarboxylation of S-adenosylmethionine provides the minopropyl modety required for spermidine biosynthesis from purescine (By similarity).

-I CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-S-adenosyl) (3-minopropyl methylsulfonium salt + CO(2).

-I CATALYTIC Belongs to the prokaryotic AdometDC family. Subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN (BY SIMILARITY).

CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).

CONVERTED TO A PYRUVOYL GROUP (BY SIMILARITY).

7659FE20A2019928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN (BY SIMILARITY).
S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
(SambC) [Contains: S-adenosylmethionine decarboxylase beta chain; S-adenosylmethionine decarboxylase alpha chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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HAMAP; MF 00464; -; 1.
HAMAP: PP0.5 TRR003826; SAMDC.
Pfam; PP0.5 AdoMetDC; 1.
Spermidine biosynthesis; Lyase; Decarboxylase; Zymogen; Pyruvate;
                                                                                                                                                                                                                                                                                                                                                 Thermotoga maritima.
Bacteria: Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
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95.0%; Score 19; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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130 AA.
PRT;
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    STANDARD;
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Y194 PYRAB
ID _Y194_PYRAB
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                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=GES / Orsay;
MEDLINE=22511545; PubMed=12622808;
Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
"An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.";
Mol. Microbiol. 47:1495-1512(2003).
-: SIMILARITY: Belongs to the UPF0146 family.
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MEDLINE=20504483; PubMed=11016950;

NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.P., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
                                                                                                                                                                                                            Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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16-OCT-2001 (Rel. 40, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (BC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
RIBH OR RIBE OR VNG0630G.
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Pred. No. 2.3e+02;
0; Mismatches 0; Indels
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PIR; G75208; G75208.
HAMAPP, MF 00341 -; 1.
InterPro; IPR00535; UPF0146.
Pfam; PF03686; UPF0146; 1.
PIRSF; PIRSF016725; UCP016725; 1.
PIRSF; PIRSF016725; UCP016725; 1.
PIRODA; PD0211130; UPF0146; 1.
SEQUENCE 131 A3; 14629 MW; D13F378187F832C3 CRC64;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0146 protein PYRAB01940.
Pyrococcus abyssi.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  NCBI_TaxID=29292;
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Q9HRMS;
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Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

"Genome sequence of Halobacterium species NRC-1.";

"Genome sequence of Halobacterium species NRC-1.";

"In the control of the formation of the part of the complex of the formation of the formati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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SPECIES-E.coli, STRAIN=K12 / MG1655;
SPECIES-E.coli, PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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YBGC OR B0736 OR C0815 OR Z0904 OR ECS0771 OR SF0561 OR S0574.
Bscherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 1; Length 133; 100.0%; Pred. No. 2.4e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; 066529; 1HQK.
HAWAP, MF 00178; -; 1.
InterPro; IRR02180; DMRL synthase.
Pfam; PF00885; DMRL synthase; 1.
ProDom; PD003664; DMRL synthase; 1.
Riboflavin biosynthesis; Transferaes; Complete proteome.
SEQUENCE 133 AA; 13719 MW; B9724DC24660DGCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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NCBI_TaxID=562, 217992, 83334, 623;
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MEDLINE=87222192; PubMed=3294803;
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Escherichia coli O157:H7, and
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P08999;
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16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
[Lumazine synthase) (Riboflavin synthase beta chain). SPECIES=S.flexmeri; STRAIN=2457T / ATCC 700930 / Serotype 2a; MRDINIB=2259074; PubMed=127049152; Wendatesan M.M., Deng W., Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna W.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner P.R.; "Complete genome sequence and comparative genomics of Shigella MEDLINE-99420866; PubMed=10493123; Poutculakis M., Takacs B.; Fourtoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.; Enrichment of low abundance proteins of Escherichia coli by hydroxyapatite chromatography."; Pactrophoreais 20:2181-2195(1999).
-I. SIMILARITY: BELONGS TO THE 4-HYDROXYBENZOYL-COA THIOESTERASE PAMILY. STRONG, TO H. INPLUENZAE H10386. . Methanobacterium thermoautotrophicum. Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter. 95.0%; Score 19; DB 1; Length 134; 100.0%; Pred. No. 2.4e+02; Live 0; Mismatches 0; Indels 18 18 BY SIMILARITY. 134 AA; 15562 MW; C44562B6EC3BE999 CRC64; 139 AA. Eccene; EG11110; ybgC.
InterPro; IPR008272; 4HBcoA_thiost_AS.
InterPro; IPR006684; 4HBcoA_thiostrse.
InterPro; IPR006683; Thioestr_supf.
Pfam; PF03061; 4HBT; ITGR00051; 1.
PROSITE; PS01328; 4HBCOA_THIOESTERASE; 1. DENTIFICATION BY MASS SPECTROMETRY. PRT; flexheri serotype 2a strain 2457T. Infect. Immun. 71:2775-2786(2003). EMBL; M16489; AAA83918.1; -.
EMBL; AE000177; AAC73830.1; -.
EMBL; AE00713; BAA35402.1; -.
EMBL; AE016757; AAN79288.1; -.
EMBL; AE005525; AAG55072.1; -.
EMBL; AE00553; BAB34194.1; -.
EMBL; AE016979; AAA72398.1; -.
EMBL; AE016979; AAP16078.1; -. Hydrolase; Complete proteome. ACT_SITE 18 Query Match
Best Local Similarity 100...
Best Local 4, Conservative STANDARD; PIR; A25980; WMEC15. PIR; C90725; C90725. PIR; D85576; D85576. 129 VAEF 132 2 VAEF 5 RISB METTH O27443; SEQUENCE RISB METTH RESULT 20 셤 COSCREDENTS ð SPECIES=E.coli; STRAIN=0157.H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796; Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; SEQUENCE FROM N.A.
SPECIES=E.Coli; STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
Shima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map."; SPECIES=S.flexmeri; STRAIN=301 / Serotype 2a; MEDLINE=22272406; PubMed=12384590; Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang G., Yuan E., Zhang Y., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441(2002). SPECIES=E.coli; STRAIN=06:H1 / CFT073 / ATCC 700928; MEDINE=238824; PubMed=12471157; MEDINE=238824; PubMed=12471157; Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; Extensive mosaic structure revealed by the complete genome sequence SEQUENCE FROM N.A.
SPECIES.E coli; STRAIN=0157:H7 / BDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551; Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkparrick H.A.,
Bosfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L.,
Grocbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Meich R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001). Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 14
                                                                                                                                                                                                                                                                   Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RISB ARCFU
028152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter J.C
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Matches
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   RAPARAPA
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REP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             Dubois J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                         SUCENCE FROM H. M. M. STRAIN-Delta H. M. Dubois STRAIN-Delta H. PubMed=9371463; Smith D.R., Doucette-Stam L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadah R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum delta!! functional analysis and comparative genomics.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 1; Length 139; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biosynthesis; Transferase; Complete proteome.
139 AA; 15464 MW; B640D8D12EE2A862 CRC64;
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the DMRL synthase family.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF0586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 AA.
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HSSP, P11998; IRVV.
HAMAP: MF 00178; -; 1.
InterPro; IPR002180; DMRL synthase.
Pfam: PF00885; DMRL synthase; 1.
ProDon; P0003664; DMRL synthase; 1.
TIGRPAMS; TIGR00114; rlbH; 1.
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Best Local Similarity
Matches 4; Conserv
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NCBI_TaxID=187420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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16-OCT-2001 (Rel. 40, Last sequence update)
18-PEB-2003 (Rel. 41, Last annotation update)
6.7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DWRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
RIBH OR RIBE OR AF2128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SERAIR=VC.16 / DSM 4304 / ATCC 49558,
MEDLINE=9804943; PubMed=9389475;
MEDLINE=98049433; PubMed=9389475;
MEDLINE=98049433; PubMed=9389475;
MEDLINE=98049433; PubMed=9389475;
MEDLINE=9804943; PubMed=980475;
Metchum K.A., Dodson R.A., Tomb J.-P., White O., Nelson K.E.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Cackehbush J., Lee N.H., Sutton G.G.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Richardson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Friji C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek, A., Zhou Overbeek R., Gocayne J.D., Weidman J.F., McDonad L., Utterback T. Cotton M.D., Sprigs T., Artiach P.F., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Masson T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the hyperthermophilic, sulphate-
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100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0; Indels
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140 AA; 16175 MW; D3B1FB3A62A05901 CRC64;
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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Nature 390:364-370(1997).
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PIR; B69323; B69323.
TIGR; AF0586; -.
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Query Match
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catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pythindinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).
-!- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflawin + 4 (1-D-ribityl)amino-2,6-dihydroxypyrimidine.
-!- PATHWAY: Riboflavin biosynthesis; last step.
-!- PATHWAY: Belongs to the DWRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MRDLINE=2036544;
MRDLINE=2036544;
Ban N., Nissen P., Hansen J., Moore P.B., Steitz T.A.;
"The complete atomic structure of the large ribosomal subunit at 2.4
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Science 289:905-920(2000).
-!- SIMILARITY: Belongs to the L13F family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE=92205119; PubMed=1840597; Kroemer W.J., Arndt E.; Kroemer W.J., Arndt E.; "Halobacterial S9 operon. Three ribosomal protein genes are cotramscribed with genes encoding a tRNA(Leu), the enolase, and putative membrane protein in the archaebacterium Haloarcula (Halobacterium) marismortui."; J. Biol. Chem. 266:24573-24579(1991).
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HAMAD, ME 00178; -; 1. D.RL_synthase.
InterPro; TPR002180; DMRL_synthase.
Pran; PF00885; DMRL synthase; 1.
ProDom; PD003664; DMRL, synthase; 1.
TIGRFAMS; TIGR00114; TibH; 1.
Riboflavin biosynthesis; Transferase; Complete proteome.
senurnce 143 AA; 15645 MW; BBA3141206905410 CRC64;
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Haloarcula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
508 ribosomal protein L13P (Hmal13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS)
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4; Conservative
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P29198;
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KRAMIN-C57BL/60; PubMed=11217851;

KRAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KRAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Jashuli W., Golbori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Chiml D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rochiml L.M., Staubil F., Suzuki R., Tomita M., Nagner L., Washio T.,

RASARI K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Baronsetein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Buronsetein M.J., Bult C., Fletcher C., Fullia M., Gariboldi M.,

Ruchone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Ruscha H., Sato K., Schoebbach C., Seya T., Shibata Y., Storch K.-F.,

M. Warshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havash'zaki Y.,
                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Nature 409:685-690(2001).
-!- FUNCTION: Implicated in the early stage of ectopic ossification.
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"DD112, a novel mouse gene implicated in the early stage of ectopic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
and for
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                                                                                                                                                                                                                                                     PDB; IRRA; 19-7UL-02.
PDB; IRRA; 19-7UL-02.
PDB; IRRD; 19-7UL-02.
PDB; IRDI; 19-7UL-02.
PDB; IMIX; 23-AUG-02.
PDB; IMIX; 23-AUG-02.
PDB; IMIX; 23-AUG-02.
PDB; IMSO; 06-SEP-02.
InterPro; IRRO05822; Ribosomal_L13.
FEAN; PP00572; Ribosomal_L13. I.
PFAM; PP00572; Ribosomal_L13. I.
PROSITE; PS00783; RIBOSOMAL_L13; I.
PROSITE; PS00783; RIBOSOMAL_L13; I.
Ribosomal protein; 3D-structure.
SEQUENCE 145 AA; 16228 MW; 069CE66662AE3BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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    Usage by
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Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Stor. No. ...
100.0%; Pred. No. ...
modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                            EMBL; M76567; AAA73097.1; -. PIR; B41715; B41715.
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Local Similarity
                      115 VAEF 118
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P11418;
                                                                                                                                                         RISB PYRAE
QBZTE3;
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                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zwickl P., Fabry S., Bogedain C., Haas A., Hensel R.;
"Glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaebacterium Pyrococcus woesel: characterization of the enzyme, cloning and sequencing of the gene, and expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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-!- SIMILARITY: Contains 3 EF-hand calcium-binding domains.
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124 124 M -> V (IN REF. 2; BAB22914).
146 148 VEN -> I (IN REF. 1).
148 AA; 16767 MW; ZAEZ2BC738ADZF9D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in GAPDH 3'region (ORF X) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Hypochetical protein.
NON TER 1 1
SEQÜENCE 148 AA; 15256 MW; 8C7E51A072DF5D50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EF-HAND 1 (POTENTIAL)
EF-HAND 2 (POTENTIAL)
EF-HAND 3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 1; Le; Pred. No. 2.6e+02;
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MEDLINE=90330536; PubMed=2165475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERMITS; PRO0450; efhand; 4.
PRINTS; PR00450; RECOVERIN.
PRODOM; PB00012; BF-hand; 2.
SMART; SM00012; BF-hand; 2.
Calcium-binding; REPBAND; 3.
CA_BIND 21 32 EF-
CA_BIND 57 68 EF-
CA_BIND 57 68
                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1931464; Calm4.
InterPro; IPR002048; EF-hand.
InterPro; IPR001125; Recoverin.
                                                                                                                                                                                                                                                                EMBL, AB036744; BAA95412.1; -. EMBL; AK009995; BAB26608.1; -. EMBL; AK009664; BAB2642.1; -. EMBL; AK003648; BAB22914.1; -.
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Best Local Similarity 100.0
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Best Local Similarity luv...
4; Conservative
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DRX PYRWO
D YORK PYRWO
C P20298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribityl-amino-2.4(1H,3H) pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
-!- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine =
- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine =
- riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
-!- PATHWAY: Riboflavin blosynthesis; last step.
-!- PATHWAY: Riboflavin blosynthesis; last step.
-!- SIMILARITY: Belongs to the DMRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                       10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6,7-dimethyl-8-ribityliumazine synthase (EC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRALT=NZ / ARCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Pitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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SEQUENCE 150 AA; 16474 MW; 73751Cl363A8AD8D CRC64;
                                                                                                                                                                                                                                                           Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Acad. Sci. U.S.A. 99:984-989(2002)
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(Rel. 12, Last sequence update)
(Rel. 42, Last annotation update)
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150 AA
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Pfam; PF00885; DMRL synthase; 1.
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TIGRFAMS; TIGR00114; ribH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE009923; AAL64819.1; -.
                                                                        .0-OCT-2003 (Rel. 42, Created)
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STANDARD;
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01-OCT-1989 (
10-OCT-2003 (
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12 VAEF 15
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P10325;
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Best Local &
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                                                                                                                              MEDLINE=89290032; PubMed=2500367;
A Galbrese L., Polticelli F., O'Neill P., Galtieri A., Barra D.,
Calabrese L., Polticelli F., O'Neill P., Galtieri A., Barra D.,
Schinian M.E., Bossa F.;
Substitution of arginine for lysine 134 alters electrostatic
T parameters of the active site in shark Cu,Zn superoxide dismutase.";
FERS Lett. 250:49-52(1989).
T PERS Lett. 250:49-52(1989).
T - FUNCTION: Destroys radicals which are normally produced within the calls and which are toxic to biological systems.
T - CATALIVITY: Sauperoxide + 2 H(+) = 0(2) + H(2)0(2).
T - CATALIVITY: Bainds 1 copper fon and 1 zinc ion per subunit.
T - SUBCELLUIAR LOCATION: Cytoplasmic.
T - SUBCONDOSO: SOGCU: 1.
T - SUBCONDOSO: SOGCU: 1.
T - SUBCONDOSO: SOGCU: 2N, 1.
T - READON: PRONONOSO: SOD CU ZN, 1.
T - READON: PRONONOSO: SOD CU ZN, 1.
T - METAL AND COMPANIONOSO: SOD CU ZN, 1.
T - METAL AND COMPANIONOSO: SOD CU ZN, 1.
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T - METAL AND COMPANIONOSO: SOD CU ZN, 1.
T - METAL STANDANIONOSO: SOD CU ZN, 1.
T - METAL
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DWRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=AICC 35092 / DSM 1617 / P2;
STRAIN=AICC 35092 / DSM 1617 / P2;
STRAIN=AICC 35092 / DSM 1617 / P2;
STRAIN=AI3132266, PubMed=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffriss A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland I.,
Superoxide dismutase [Cu-Zn] (EC 1.15.1.1).
Prionace glauca (Blue shark).
Briaryyota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeonorphii; Galeoidea; Carcharhiniformes; Carcharhinidae; Prionace.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 1; Length 152; 100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6617642A4F23C5AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COPPER AND ZINC.
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55 1
152 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                     NCBI_TaxID=7815;
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                                                                                                                       SEQUENCE
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Q980B5;
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Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaecon Sulfolbous solfataricus P2.";
Proc. Natl. Acad. Sci. U. S.A. 98:735-7840(2001).
-1- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-
ribityl-amino-2.4 (1H.3H)-pyrimidinhedione and L-3.4-dihydrohy.2-
butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-
amino-2,4 (HH.3H)-pyrimidinedione with L-3,4-dihydrohy-2-
butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
riboflavin + 1-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
-!- PATHWAY: Riboflavin biosynthesis; last step.
-!- SIMILARITY: Belongs to the DMRL synthase family.
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STRAINER / KW20 / ATCC 51907;
STRAINER - KW20 / WZ0 / ATCC 51907;
STRAINE - STRAINER - STRA
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01-NOV-1995 (Rel. 32, Last sequence update)
110-CTT-2003 (Rel. 42, Last annotation update)
Outer membrane lipoprotein PCP precursor (15 kDa lipoprotein) (PAL
cross-reacting lipoprotein).
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Pasteurellaceae; Haemophilus.
NCBL_TaxID=727;
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SEQUENCE 154 AA; 17247 MM; ADFA9E6A2C723210 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 1; L. Pred. No. 2.7e+02;
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100.0%; Pred. No. ...
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HAMAP; MF 00178; -; 1.

InterPro; IPR002180; DMRL synthase.
Pfam; PF00895; DMRL synthase; 1.

ProDom; PD003664; DMRL synthase; 1.

TIGRFAMS; TIGR00114; ribH; 1.
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les 4; Conserv
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30-MAY-2000 (Rel. 39, Last sequence update)
15-MAY-2004 (Rel. 43, Last annotation update)
15-MAY-2004 (Rel. 43, Last annotation update)
Taraxacum officinale (Common dandelion).
Taraxacum officinale (Common dandelion).
Spermatyota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicoryledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Geoghagen N.S.M., Geoghagen N.S.M., Vencer J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Vencer J.C.;
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                                                                                                                                                                                                                             Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Complete proteome; Palmitate.
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S-diacylglycerol cysteine.
S-LOABEVF -> VAGREVRI (IN REF.
D7880327FCF0C985 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 155;
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TISSUE=Root;

Xu X.-Y., Bewley J.D., Greenwood J.S.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the BetVI family.
                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLYB AND TO Y.ENTEROCOLITICA PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 1; Le 100.0%; Pred. No. 2.7e+02; Live 0; Mismatches 0;
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155 AA; 15425 MW;
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Best Local Similarity
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049065;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine. PATHWAY: Riboflavin biosynthesis; last step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawarabayasi Y., Hino Y., Horikawa H., Jin.no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Maguda S., Yanagii M., Nishimura M., Yamagishi A.,
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                      10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation spathase)
(Iumazine synthase) (Riboflavin synthase beta chain).
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                     ..
                                                                                                                                                       Length 157;
                                         Interpro; IPR000916; Bet v I.
Pfam; PF00407; Bet v I; I.
PRINTS; PR00634; BETALLERGEN.
PROSITE; PS00451; PATHOGENESIS_BETVI; 1.
Allergen; Plant defense; Pathogenesis-related protein.
SEQUENCE 157 AA; 17040 MW; 5892AB8593ABA7E0 CRC64;

    -!- SIMILARITY: Belongs to the DMRL synthase family.

                                                                                                                                                     95.0%; Score 19; DB 1; Le
100.0%; Pred. No. 2.8e+02;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                               157 AA.
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InterPro; IPR00218; DWRL synthase.
JEam; PF00885; DWRL synthase; 1.
ProDom; PD003664; DWRL synthase; 1.
TIGRFAMS; TIGR00114; rIDH; 1.
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MEDLINE=21456156; PubMed=11572479;
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HAMAP; MF_00178; -; 1.
              EMBL; AF036931; AAB92255.1; -.
HSSP; O24248; 1E09.
                                                                                                                                      Query Match
Best Local Similarity 10v...
4; Conservative
                                                                                                                                                                                                                                                                                                                               STANDARD;
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ID RISB SULTO
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Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000). 01-0CT-1993 (Rel. 27, Created) 01-0CT-1993 (Rel. 27, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) UTRS protein (Unknown transcript 5 protein). UTRS OR YEL035C OR SYGP-ORF27. EMBL; X04269; CAA27820.1; -. EMBL; AR003718; AAF55436.1; -. PIR; A24504; A24504. FlyBase; FBGn0003375; Sgs5. STANDARD; Nature 387:78-81(1997). SEQUENCE FROM N.A. STRAIN=S288C / AB972; Local Similarity SEQUENCE FROM N.A. 114 VAEF 117 NCBI_TaxID=4932; 2 VAEF 5 UTRS YEAST P32630; Query Match Signal. Best Loc Matches UTRS_YEAST RESULT 33 SPET WARRANGE COCCOCCEPTA SOLVE SOLV ઠ MEDLINE=2019606; Punded=1073132;

MEDLINE=2019606; Punded=1073132;

Amanatides P.G., Scherer S.E., Itolt R.A., Gable R.F.,

Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Workman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.H.C., Blaze? B.G., Change M., Pfelifer B.D.,

Abril J.F., Agbayani A., An H. J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Beasley B.M.,

Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Beasley B.M.,

Ballew R.M., Basu A., Butler H., Cadlew B., Center A., Chandra I.,

Borkova D., Botchan M.R., Bouck J., Brokstein P. Brottier P.,

Borkova D., Botchan M.R., Bouck J., Brokstein P. Brottier P.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Borkova D., Botchar A., Deng Z., Mays A.D., Dew I., Diletz S.M.,

Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Diletz S.M.,

A Burbin K.J., Evangelista C., Ferrac C., Ferriera S., Placks W., Glasser K.,

Codson K., Doup L.E., Downes M., Dugan-Rocha S., Placks W., Glasser K.,

A Gong F., Gorrell J. H., Gu Z., Guan P., Harris M.,

Hostin D., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,

A lastin D., Houston K.A., Howland T.J., Hernandez J.R., Katchum K.A.,

A lastin D., Houston K.A., Howland T.J., Weil D.J., Lai Z.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Mount S.M., Mulbina N.V., Mobarry C., Morris J., Mosher D.,

Rollson D.R., Nelson K.A., Li J.H., H. J., Liang Y., Lin X.,

Mang Z.-Y., Massarman D.A., Weiner R., Vang A., Wang X.,

Mang Z.-Y., Wassarman D.A., Weiner R., Vang A., Wang X.,

Milliams S.M., Woodeg T., Worley K.C., Wu D., Yang S., Zalon Z.,

A halliams S.M., Woodeg T., Worley K.C., Wu D., Yang S., Zalon X.,

Milliams S.M., Woodeg T., Wooley W., Zhou Y., Zhou S., Zhou S., Zhou X., Zhou X., Zhon X., Zhon X., Zhon X., Zhou X., Zhou X., Zhou X., Zhou X., Zhou X., Zhon X., ö Gaps STRAIN=Cregon-R;
MEDLINE=87086754; PubMed=3098981;
Shore E.M., Guild G.M.;
"Larval salivary gland secretion proteins in Drosophila structural analysis of the Sgs-5 gene.";
J. Mol. Biol. 190:149-158(1986). ô Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila. Length 157; Query Match
95.0%; Score 19; DB 1; Length 157
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels Riboflavin biosynthesis; Transferase; Complete proteome. SEQUENCE 157 AA; 17501 MW; 529558077E164A18 CRC64; PRT; 163 AA

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MEDLINE=94016558; PubMed=8411151;
Melnick L., Sherman F.;
Melnick L., Sherman F.;
Melnick L., Sherman F.;
of Saccharomyces cerevisiae share a common ancestry.";
J. Mol. Biol. 233:372-388(1993).
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MEDIATE-273264; PubMed-9169868;
MEDIATE-973264; PubMed-9169868;
Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Garman E., Hartzell G., Hauricke-Smith S., Hyman R., Komp C., Lashkari D., Lew H. Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Pecel F.X., Roberts D., Sehl P., Scharam S., Shogren T., Shogton P., Santh V., Taylor P., Wei Stockets D., Davis R.W., Kaylor P., Chen M., Davis R.W., Kaylor P., Wei Y., Botstein D., Davis R.W., K., Linhen L., Laston C., Davis R.W., M., Taylor P., Wei Y., Botstein D., Davis R.W., Linhen L., Roberts D., Barland C., Pecel J., Wei Y., Botstein D., Davis R.W., Linhen L., Mensell R.W., R.W., Linhen L., Mensell R.W., R.W., Laston R.W., R.
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Eukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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CHAIN 19 163 SALIVARY GLUE PROTEIN SGS-5.
SEQUENCE 163 AA, 18821 MW; 3A476FID3B06D864 CRC64;
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CONFLICT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      June 1 maintaining endothelial survival deprivation. May function in the response of hemopolatic cells to external signals and in maintaining endothelial survival during infection.

1. SUBCELLULAR LOCATION: Intracellular.

1. SUBCELLULAR LOCATION: Intracellular.

1. TISSUE SPECITY: Expressed in hemopoietic tissues, including bone marrow, spleen and thymus.

1. INDUCTION: By granulocyte-macrophage colony-stimulating factor and LPS in macrophages.

2. SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

2. SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                 01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl-2-related protein Al (BFL-1 protein) (Hemopoietic-specific early
response protein) (Al-A).
BCL2Al OR BCL2AlA OR BFL1 OR Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CBA/J; TISSUE=Bone marrow;
MEDLINE=93346743; PubMed=8345191;
Lin E.Y., Orlofsky A., Berger M.S., Prystowsky M.B.;
"Characterization of Al, a novel hemopoietic-specific early-response gene with sequence similarity to bcl-2.";
J. Immunol. 151:1979-1988(1993).
                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Multiple gene duplication and expression of mouse bcl-2-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98307518; PubMed-9645611;
Hatakeyama S., Hamasaki A., Negishi I., Loh D.Y., Sendo F.,
Nakayama K., Nakayama K.-I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37AD35818E756488 CRC64;
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Similarity 100.0%; Pred. No. 3e+02;
4; Conservative 0; Mismatches 0;
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SMOSITE; BS50062; BCL2_PAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
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EMBL; U23774; AAB97953.1; -
EMBL; U23773; AAB97953.1; JOINED.
PIR; 149449; 149449.
HSSP; Q07817; 1MAZ.
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InterPro; IPR000712; Bcl2_BH.
InterPro; IPR002475; BCL2_family.
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77 97
132 147 BH2
172 AA; 19914 MW; ?
                                                                                    (Rel. 31, Created)
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Best Local Similarity
Matches 4; Conserv
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                                                                                 01-FEB-1995
                  BFL1 MOUSE
Q07440;
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-!- FUNCTION: This protein is essential for replication of the chromosome. It is also involved in DNA recombination and repair (By similarity).
-!- SIMILARITY: Contains 1 SSB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Firellula sp. strain 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSB RHOBA STANDARD; PRT; 169 AA.
P59532; Q7UKX3;
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
55-MAR-2004 (Rel. 43, Last annotation update)
SSB OR RB9917.
Rhodopirellula baltica.
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DNA-binding; DNA repair; DNA replication; Complete proteome.
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Pred. No. 2.9e+02;
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166 AA; 19335 MW; ASBEEBDOFA6D3DEA CRC64;
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100.0%; Pred. No. 2...
0; Mismatches
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STRAIN=1;
MEDLINE=22735913; PubMed=12835416;
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EMBL; L22173; AAA34936.1; --
EMBL; S65564 AAAD13970.1; --
EMBL; S65120; AAB28442.1; --
EMBL; U18779; AAB65007.1; --
EMBL; S55050; S55050; GermOnline; 139039; --
SGD; S0000761; UTR5.
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nes 4; Conservative
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SULT 35

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[2]
SEQUENCE FROM N.A.
                                                                                      SEQUENCE FROM N.A.
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                                               SEQUENCE FROM N.A.
    122 VAEF 125
                                          NCBI_TaxID=9606;
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                HUMAN
           T 36
HUMAN
                PUFFFFFFFFSVVVX4FFF774VX4FFF35PVX45FF35PVX45FF
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TISSUE SPECIFICITY: Seems to be restricted to the hematopoietic PRT; PROSITE; PS50062; BCL2 FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. 20132 MW; EMBL; BC016281; AAH16281.1; -. EMBL; U29680; AAC50438.1; -. EMBL; U27467; AAC50288.1; -. EMBL; Y09397; CAA70566.1; -. Conservative PIR; 139055; 139055. HSSP; P53563; 1AF3. Genew; HGNC:991; BCLZA1. STANDARD; 33 97 147 72 24 77 132 1 72 107 175 AA; SMART; SM00337; BCL; Local Similarity SECUENCE FROM N.A. 122 VAÈF 125 NCBI_TaxID=8400; 2 VAEF 5 FRI2_RANCA P07798; 4. Apoptosis. DOMAIN CONFLICT CONFLICT Query Match DOMAIN RANCA Best Loc Matches RESULT 37 <del>|</del> HERRER REPORTED THE SERVICE OF THE S ద ઠે TISSUB-Skin;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; MEDLINE N., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Uddin T.B., Toshiyuki S., Carninot P., Parage C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murxip D.M., Sodergren E.J., Lu X., Gibbs R.A., Character S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murxip D.M., Madan A., Rodrigues S., Sanchez A., Mara M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schmutz J., Marra M.A.;

Medneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Marra M.A.;

Medneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Marra M.A.;

Medneration and initial analysis of more than 15,000 full-length function in the response of hemopoietic cells to external signals and in the response of hemopoietic cells to external signals and in the response of hemopoietic cells to external signals and in the response of hemopoietic cells to external signals and in the response of hemopoietic cells to external signals and in the response of hemopoietic cells to external signals and in the response of hemopoietic cells to external signals and the sequences induced by IL-3 deprivation. (By external signals and the sequences induced by IL-3 deprivation (By external signals and the sequences induced by IL-3 deprivation (By external signals and the sequences induced by IL-3 deprivation (By external signals and the seq "GRS, a novel member of the Bcl-2 gene family, is highly expressed in multiple cancer cell lines and in normal leukocytes."; Oncogene 14:997-1001(1997). 016548; 099524; 010V-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last sequence update) Bcl-2-related protein Al (BFL-1 protein) (Hemopoietic-specific early response protein) (GRS protein). Homos appiens (Human). Homos appiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. TISSUE-Liver;
MEDLINE=96068995; PubMed=7478596;
MEDLINE=96068995; PubMed=7478596;
MEDLINE=96068995; Park I.-C., Yun J.W., Sung Y.C., Hong S.-I., Shin H.-S.;
"A novel Bcl-2 related gene, Bfl-1, is overexpressed in stomach cancer and preferentially expressed in bone marrow.";
Oncogene 11:1693-1698(1995). MEDLINE=97203281; PubMed=9050999; Remny J.J., Knobloch T.J., Augustus M., Carter K.C., Rosen C.A., Lang J.C.; "GRS, a novel member of the Bcl-2 gene family, is highly expressed Karsan A., Yee E., Kaushansky K., Harlan J.M.; Groing of human Bcl-2 homologue: inflammatory cytokines induce human Al in cultured endothelial cells."; Blood 87:3089-3096(1996). 175 AA similarity).
SUBCELLULAR LOCATION: Intracellular. TISSUE-Umbilical vein; MEDLINE-96184764; PubMed-8605321; STANDARD; Ŋ 2 VAEF

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-- INDUCTION: By phorbol ester and inflammatory cytokines, such as TNF-alpha, or IL-1-beta, but not by growth factors.

-- SIMILARITY: Contains 1 BC-2 homology 1 (BH1) domain.

-- SIMILARITY: Belongs to the BC1-2 family. Gaps 01.AUG-1988 (Rel. 08, Created)
01.AUG-1988 (Rel. 08, Last sequence update)
10.0CT-2003 (Rel. 42, Last annotation update)
Ferritin, middle subunit (Ferritin M) (Ferritin X) (Ferritin H').
Rana catesbelana (Bull frog). Rana catesbeiana (Bull frog). Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi; Amphibia; Batrachia, Anura, Neobatrachia; Ranoidea; Ranidae; Rana ö 95.0%; Score 19; DB 1; Length 175; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels N -> T (IN REF. 3). Q -> H (IN REF. 3). 329D98AF2BE07A0D CRC64; MIM; 601056; -... GO; GO: 0008189; F: apoptosis inhibitor activity; TAS. GO; GO: 00008189; F: apoptosis; TAS. GO; GO: 00006916; F: anti-apoptosis; TAS. InterPro; IPR000712; BCI2_family. PF00452; BCI2_family. 176 AA. ALA/PRO-RICH.

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                                                                                                                                                                                                                                                                  Fuller T.E., Kennedy M.J., Lowery D.E.,
"Identification of Pasteurella multocida virulence genes in a
septicemic mouse model using signature-tagged mutagenesis.";
submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEBB PASMU STANDARD; PRT; 178 AA.
Q9LGB3; P57804;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2011 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Disulfide bond formation protein B (Disulfide oxidoreductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales.
Pasteurellaceae, Pasteurella.
                                                                                                                                                Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; Pf00466; Ribosomal L10; I.
PROSITE; PS01109; RIBOSONAL L10; FALSE NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 177 AA; 19591 NW; SODDCF896EF6F4E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 1; Le
Pred. No. 3.1e+02;
Z8-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
20-FEB-2003 (Rel. 41, Last annotation update)
508 ribosomal protein Li0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Scor.
100.0%; Pred. No. s...
                                                                                                                                                                           Bacteria; Firmicutes; Clostridia; Thermoanaer
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP, MF 00362; -; 1.
Interpro; IPR001790; Ribosomal L10.
Interpro; IPR002363; Ribosomal L10eub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE013173; AAM25445.1; -.
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Best Local Similarity 100...
---- 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                      NCBI_TaxID=119072;
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         Gaps
                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: THERE ARE THREE TYPES OF FERRITIN SUBUNITS: L, MAND H CHAINS IN AMPHIBIA.
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                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the ferritin family.
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PROSITE; PS00540; FERRITIN 1; 1.
PROSITE; PS00204; FERRITIN 2; 1.
PROSITE; PS50905; FERRITIN LIKE; 1.
Iron storage; 1.
DOMAIN 156
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100.0%; Pred. No. 3...
0; Mismatches
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PDB; 1MFR; 22-JUN-99.
InterPro; PR001519; Ferritin.
InterPro; IPR008331; Ferritin.Dps.
InterPro; IPR008331; Ferritin.Dps.
Pfam; PF00210; ferritin.like.
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Best Local S
Matches 4
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TURN
HELIX
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177 AA.

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STANDARD;

SSULT 38 510 THETN 7 RL10 THETN

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Gaps

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Length 177; 0; Indels us-09-594-978a-3.rsp

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                                                             SIMILATILY/.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
FUNCTION: Required for disulfide bond formation in some periplasmic proteins. Acts by oxidizing the dsbA protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase, Redox-active center, Transport, Electron tra
Chaperone, Transmembrane, Inner membrane, Complete proteome.
DOMAIN 14 14 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
D2C45BB73B31F0BC CRC64;
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                                                                                                     (By similarity). SIMILARITY: Belongs to the dsbB family.
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InterPro, IPR003752, DsbB.
Pfam, PF02600, DsbB; 1.
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105
178 AA;
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Gaps ô Length 178; 0; Indels Score 19; DB 1; Le Pred. No. 3.1e+02; 95.0%; Scort 100.0%; Pred. No. J. O. Mismatches 4; Conservative Query Match Best Local Similarity Matches

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ESULT 40 SM5 DROME

ESMS_DROME STANDARD; PRT; 178 AA. P13096; Q9VB18; Created) 01-JAN-1990 (Rel. 13, Created) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Enhancer of split m5 protein (E(spl)m5). Drosophila melanogaster (Fruit fly). OURFERZOUCOXZEXHEHZAUX4444

Eukaryota; Metazoa; Arthropoda; Héxapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

MEDLINE-89231619; PubMed=2540957; Atlanta C., Knust E., Tlatter K., Campos-Ortega J.A.; Calcosly related transcripts encoded by the neurogenic gene complex enhancer of split of Drosophila melanogaster."; SEQUENCE FROM N.A.

STRAIN=Berkeley;
MEDLINE=20196066; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., EMBO J. 8:203-210(1989) SEQUENCE FROM N.A.

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
And K.H., Doyle C., Baxter E.G., Helt G., Nalson C.R., Miklos G.L.G.,
Balluw R.M., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,
Balluw R.M., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,
Beeson K.Y., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,
Beeson K.Y., Basu A., Bauck J., Brandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davendort L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davendort L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferriera S., Pleischmann W.,
R. Durbin K.J., Brongelista C.C., Ferraz C., Ferriera S., Pleischmann M.,
R. Durbin K.J., Brongelista C.C., Ferraz C., Ferriera S., Fleischmann M.,
R. Glodek A., Gong F., Garg N., Bidmar T.J., Harris M.,
Alostin D., Houston K.J., Heiman T.J., Herrandez J.R., Houck J.,
Alatin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alatin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alatin M., Maurph B., McIntosh T.C., McIeod M.P., Moshrefa N.,
Merkulov G., Milshina N.V., Mobarty G., Moshrefi A.,
Mount S.M., May M., Murphy B., Murphy D., Muznhy D., Muznhy D., Mozhrefa F., Shen H.,
R. Ahazzolo M., Pittuan G.S., Pan S., Pollard J., Pholy M., Mang X.,
R. Alater B.C., Siden-Kiamos I., Staplero M., Skupski M.P., Smith T.,
Sheng X.H., Zhong F.N., Zhong M., Zhou X., Smith H.O.,
R. Zheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,
R. Zheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,
R. Zheng C. M., Welsenbed T.C., Salence E., R., Merger B.C., Sidence D. Spith B. Shoul S., Zhong M., Zhou X., Zhu S., Zhu X., MEDLINE=95094252; PubMed=8001118; Paroush Z., Finley R.L. Jr., Kidd T., Wainwright S.M., Ingham P.W., Paroush Z., Finley R.L. Jr., Kidd T., Wainwright S.M., Ingham P.W., Ish-Horowicz D.; Redt R., Ish-Horowicz D.; "Groucho is required for Drosophila neurogenesis, segmentation, and sex determination and interacts directly with hairy-related bHLH SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain. SIMILARITY: Contains 1 orange domain. Hairy-related proteins. proteins."; Cell 79:805-815(1994). 

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EMBL; X16552; CAA34552.1; .. EMBL; AE003754; AAF56552.1; EMBL; AE003754; AAFE PIR; S03629; S03629. 178 AA; 19319 MW; 378A4F200240D924 CRC64;

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SEQUENCE
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                                                                                   Query Match
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                                                                                                                                  Best Loc
Matches
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DIT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
KIENK H.-P., Clayton R.J., Tomb M., Hickey B.K., Peterson J.D.,
KIChardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Kichardson D.L., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I.,
Peterson R., Gocayne J.D., Waidman J.F., McDonald'L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
                                                                                   CONTROL OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 1; Length 178; 100.0%; Pred. No. 3.1e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001027; ABB0141.1; -.
PIR; E69389.
TIGR; AF118; -.
Hypothetical protein; Signal; Complete proteome.
SIGNAL
1 20
HYPOTHETICAL PROTEIN AF1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 129 CRANGE.
175 178 WRPW MOTIF.
178 AA; 19923 MW; 19363D0F6043C84F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea, Euryarchaeota, Archaeoglobi, Archaeoglobales;
Archaeoglobaceae, Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AFI118 precursor.
AF1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation, Repressor.
DNA_BIND 19 33 BASIC D
DOMAIN 34 74 HELIX-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4, Conservative
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Nature 390:364-370(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 VAEF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 ARCFU
18 ARCFU
19147:
16-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=35000HP / ATCC 700724;

Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,

Adunson L., Nguyen D., Wang J., Forst C., Hood L.;

Johnson L., Nguyen D., Wang J., Forst C., Hood L.;

The complete genome sequence of Haemophilus ducreyi.";

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

I. TUNCTION: Catalyzes a salvage reaction resulting in the formation of AMP, that is energically less costly than de novo synthesis.

C. I. CATALYTIC ACTIVITY: AMP + diphosphate = adentine + 5-phospho-alpha-

D. PAHWAY: Putine salvage.

C. I. STHUMAY: Homodimer (By similarity).

C. SUBUNIT: Homodimer (By similarity).

C. SUBURIARATY: Belongs to the purine/pyrimidine

phosphoribosyltransferase family.
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                                                                  Gaps
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TIGRFAMs; TIGR01090; apt; 1.
TIGRFAMs; TIGR01090; pt; 1.
Transfers; S00103; PIR-PY PR TRANSFER; 1.
Transferae; Glycosyltransferae; Purine salvage; Complete proteome. SEQUENCE 179 AA; 19315 MW; 13A1DAFDC13560DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 1; Length 179; 100.0%; Pred. No. 3.1e+02; Aismatches 0; Indels
Length 178;
                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          E-WR-2004 (Rel. 43, Created)
15-WR-2004 (Rel. 43, Last sequence update)
15-WR-2004 (Rel. 43, Last amotation update)
43-Mare and Rel. 43, Last amotation update)
Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT)
APT OR HD1818
95.0%; Score 19; DB 1; Lv
100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HANAP; MF 00004; -; 1.
INCETPLO; IPR005764; Ade phspho_trans.
INTERPLO; IPR002375; Pr/py_rp_transf.
INTERPLO; IPR000836; PRTransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE017156; AAP96568.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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                                    Local Similarity 100.
ses 4; Conservative
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus ducreyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                              155 VAEF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 VARF 48
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                                                                                                                               2 VAEF 5
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RETB BOVIN
ID RETB BOVIN
AC P18902;
                                                                                                                                                                                                                                                                                                                                                     APT HAEDU
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SIMILARITY SIMILARITY

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PRINTS; PRO0179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Lipocalin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR002345; Lipocalin.
InterPro, IPR000566; Lipocln_cytFABP
Pfam; PF00061; lipocalin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, $65585, AAB28336.1; -... PIR, 146955, 146955. PIR, 533186; $13186. PDB, 1ERB, 31-JAN-94. PDB, 1HBP, 31-JAN-94. PDB, 1HBQ, 31-JAN-94. PDB, 1FEL, 01-NOV-94. PDB, 1FEL, 01-NOV-94. PDB, 1FEN; 01-NOV-94.
                                                              NCBI_TaxID=9913;
                                                                            SEQUENCE
                                                                                                                        data."
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95.0%; Score 19; DB 1; Le
ilarity 100.0%; Pred. No. 3.2e+02;
Conservative 0; Mismatches 0;
                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
3D-structure.
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNAA WOLSP
ID DNAA WOLSP
AC P35907;
                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                           STRAND
TURN
STRAND
TURN
STRAND
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STRAND
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                                                                                           TRAND
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                                                    HELIX
TURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The bovine plasma retinol-binding protein. Amino acid sequence, interaction with transthyretin, crystallization and preliminary X-ray
                                                                                                                                                                                                                                                                                                                  "Expression and cellular localization of retinol-binding protein messenger ribonucleic acid in bovine blastocysts and extraembryonic membranes.";
                                                                  Bos taurus (Bovine).
Wakaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Cetarriodactyla; Ruminantia, Pecora, Bovoidea;
Bovidae; Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY.

MEDLINE-2922293, PubMed=1623143;

Monaco H.L., Zanotti G.,

"Three-dimensional structure and active site of three hydrophobic molecule-binding proteins with significant amino acid sequence similarity.";

Biopolymers 32:457-465(1992).
                                                                                                                                                                                                                                                            [2]
SEQUENCE OF 52-183 FROM N.A.
SEQUENCE OF 52-183 FROM N.A.
SEQUENCE = 93385352; PubMed=8373966;
Liu K.H., Dore J.J. Jr., Roberts M.P., Krishnan R., Hopkins F.M., Godkin J.D.;
                                                                                                                                                                         Berni R., Stoppini M., Zapponi M.C., Meloni M.L., Monaco H.L.,
Zanotti G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kidney glomeruli.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the lipocalin family.
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein (PRBP) (RBP).
                                                                                                                                                                                                                                               Eur. J. Biochem. 192:507-513 (1990).
                                                                                                                                                               MEDLINE #91006139; PubMed = 2209607;
                                                                                                                                                                                                                                                                                                                                                                      Biol. Reprod. 49:393-400(1993).
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Gaps

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0, Indels

Length 183;

21068 MW; D6BA064CB9E67C09 CRC64;

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                                                                                                                                                       Wolbachia sp.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Wolbachieae; Wolbachia.
NCBI_TaxID=956;
                       01-JTN-1994 (Rel. 29, Created)
01-JTN-1994 (Rel. 29, Last sequence update)
01-JTN-1994 (Rel. 21, Last amoutation update)
28-FEB-2003 (Rel. 41, Last amoutation update)
Chromosomal replication initiator protein dnaA (Fragment)
186 AA
PRT;
 STANDARD;
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Pfam; PF00355; Rieske; 1.
PRINTS; PR00165; RIESKE.
TRIGRAMS; TIGRO146; RIESKE.
TIGRIAMS; TIGRO1409; TAT signal_seq; 1.
PROSITE; PS00199; RIESKE_1; 1.
PROSITE; PS00200; RIESKE_2; 1.
Electron transport; Inner membrane; Transmembrane; Metal-binding; Iron-sulfur; Iron; 2Fe-2S; Oxidoreductase.
TRANSMEM 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanococcus jannaschii.
    InterPro; IPR006311; Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBUNIT: Homodimer.
                                                                                                                                                                                                                 137 1
190 AA;
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                        2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                             NTPA METUA
057679;
                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                     METAL
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                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Ubiquinol-cytochrome C reductase iron-sulfur subunit (EC 1.10.2.2)
(Rieske iron-sulfur protein) (RISP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ferrocytochrome c.
COFACTOR: Binds 1 2Fe-2S iron sulfur cluster per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: The Rieske protein is a high potential 2Fe-2S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: The main subunits of complex b-cl are: cytochrome cytochrome cl and the Rieske protein.
SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paracoccus denitrificans.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
                                                                                                                                                                                     Length 186;
                                                                                                                                                       186 AA; 21283 MW; C423C06CEFFB0459 CRC64;
                                                                                                                                                                                95.0%; Score 19; DB 1; Le
100.0%; Pred. No. 3.3e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein. SIMILARITY: Belongs to the Rieske family.
EMBL, Z28981, CAA82285.1; -.
PIR, S39317, S39317.
HAMAP, MF-00377; -1.
InterPro, IPR001957; Bac_DnaA.
Pfam; PF00308; bac_dnaA; 1.
PRINTS; PR00651; DNAA.
PROSITE; PS01008; DNAA, PARTIAL.
DNA replication; DNA-binding; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                        190 AA.
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Interpro; IPR005806; Rieske dom.
Interpro; IPR006317; Rieske_proteo.
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EMBL; X05799; CAA29243.1; -.
PIR; A29413; A29413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhodobacteraceae; Paracoccus
NCBI_TaxID=266;
                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                              134 VAEF 137
                                                                                                                                                                                                                                               2 VAEF 5
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UCRI_PARDE

P05417;
                                                                                                                                                     SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-!- FUNCTION: CAN EFFICIENTLY HYDROLYZE NONSTANDARD NUCLEOTIDES SUCH
AS XTP TO XMP ON ITP TO IMP, BUT NOT THE STANDARD NUCLEOTIDES. XTP
IS THE BEST SUBSTRAITE.
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087.
Sult G.J., White O., Oleen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Rerlavage A.R., Dougherty B.A., Tomb. J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Feterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=99332061; PubMed=10404228;
Hwang K.Y., Chung J.H., Kim S.-H., Han Y.S., Cho Y.;
"Structure-based identification of a novel NTPase from Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                           Gaps
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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10-0CT-2003 (Rel. 42, Last annotation update)
Nucleoside-triphosphatase (BC 3.6.1.15) (Nucleoside triphosphate
phosphohydrolase) (NTPase).
                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                95.0%; Score 19; DB 1; Length 190; 100.0%; Pred. No. 3.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                      154 BY SIMILARITY.
20299 MW; F83F5D9A9C1FBEE4 CRC64;
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   IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
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InterPro; IPR006120; HTH 7.
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Best Local Similarity
4, Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=C-125 / JCM 9153;
MEDLINE220512582; Pubmed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 1; Length 193; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=86665;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HAM1 protein homolog 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 AA
                                                                                                                       PIR; C64328; C64328.
PDB; 1B78; 28-JAN-00.
PDB; AMJP; 28-JAN-00.
TICR; MJ0226; --
HAMAP; MF_01405; arypical; 1.
InterPro; IFR002637; Hamlp_like.
Pfam; PF01725; Hamlp_like.
TICRFAMS; TIGR00042; TIGR00042; 1.
                                                                                                  EMBL; U67478; AAB98211.1; -. PIR; C64328;
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193 AA;
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Best Local Similarity
Matches 4; Conserv
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Д9К8<u>Б</u>9;
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HELIX
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     PAFFFEXXXXX397X444
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F. Tromplete general sequence of the shighlightic heartillus subtillus.

R. Michael Andreas sequence of the shighlightic heartillus subtillus.

R. Michael Andreas and genomic sequence comparison with Beatillus subtillus.

1. SAILARITY: Balongs to the HAM INTERS Emmily.

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196 AA; 21852 MW;
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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SEQUENCE FROM N.A.
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PINR ECOLI
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InterPro; IPR006118; Recombinase.
InterPro; IRR006119; resolvase_N.
Pfam; PP002796; HTH 7; 1.
Pfam; PP00239; resolvase; 1.
PROSITE; PS00397; RECOMBINASES 1; 1.
PROSITE; PS00397; RECOMBINASES 2; 1.
PROSITE; PS00398; RECOMBINASES 2; 1.
DNA recombination; DNA integration; DNA-binding; Transposable element.
ACT_SITE 11 11 STRANSIENT COVALENT LINKAGE TO DNA DURING STRANSIENT COVALENT LINKAGE TO DNA DURING (BY SIMILARITY).

189 HTH-H MOTIF (PROBABLE).

199 HTH-H MOTIF (PROBABLE).

199 HTH-H MOTIF (PROBABLE).

199 HTH-H MOTIF (PROBABLE).
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MIDLINE=97251357; PubMed=9097039;

MIDLINE=97251357; PubMed=9097039;

Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,

Kasai H., Kashimoto K., Kimtara S., Kitakwa M., Kitagawa M.,

Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,

Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,

Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,

Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,

Takemoto K., Dawa sequence of the Escherichia coli K-12 genome

corresponding to the 28.0-40.1 min region on the linkage map.";

DNA Res. 3:363-377(1996).

-- SIMILARITY: Belongs to the site-specific recombinase resolvase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Putative DNA-invertase from lambdoid prophage Qin.
PINQ OR B1545.
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EMBL; D90799; BAA15249.1; -.
PIR; D64909; D64909.
HSSP; P03012; 2RSL.
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NO ECOLI

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BcoGene; BG13824; pinQ.
InterPro; IPR006118; Recombinase.
InterPro; IPR006118; Recombinase.
InterPro; IPR006118; Recombinase.
InterPro; IPR006119; resolvase_N.
Pfam; PF002796; HTH 7; 1.
Pfam; PF00239; RECOMBINASES_1; FALSE_NEG.
PROSITE; PS00399; RECOMBINASES_2; 1.
Hypothetical protein; DNA recombination; DNA integration; DNA-binding; DNA invertase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                      TRANSIENT COVALENT LINKAGE TO DNA DURING STRAND CLEAVAGE AND REJOINING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=06.HI / CFT073 / ATCC 700928;
MEDLINE=2388234; Pubmed=12471157;
WHICH R.A., BULLINE L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perra N.T., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perra N.T., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perra N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
McDil W. Donnenberg M.S., Blattner F.R.;
Percan Secherichia coli., 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 2017, 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESPOENCE FROM N.A.
SSTEALNEKLZ / MGJ655,
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Goeden M.A., Rose D.J., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=562, 217992;
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Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7CF47F6D88DBD497 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last amocation update)
Putative DNA-invertase from lambdoid prophage Rac.
PINR OR B1374 OR C3146.
Escherichia coli, and
Escherichia coli, 066.
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WEDLINE=93315143; PubMed=7686882;
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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01-070-1989 (Rel. 11, Last sequence update)
10-070-2003 (Rel. 2) Last annotation update)
17-anscriptional regulatory protein uhpA.
UHPA OR B1669 OR C4593 OR Z5159 OR ECS4606 OR SF3792 OR S3976.
Bscherichia coli,
Escherichia coli 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=E.coli;
MEDLINE=87279903; PubMed=3301805;
Priedrich M.J., Kadner R.J.;
Filedrich M.J., Radner E.J.;
Filedrich Bequence of the uhp region of Escherichia coli.";
J. Bacteriol. 169:3556-3563 (1987).
                                                                                                                                                                                                                                                                                               TRANSIENT COVALENT LINKAGE TO STRAND CLEAVAGE AND REJOINING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 1; Length 196;
Pred. No. 3.4e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  643A62BC940B29A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 AA
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SPECIES=E.coli; STRAIN=K12 / MG1655;
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NCBI_TaxID=562, 217992, 83334, 623;
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100.0%; Pred
0; M
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MEDLINE=92234930; PubMed=1569007;
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                                                                                                                                                                                                                                                                                                                                   196 AA; 21908 MW;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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D UHPA_ECOLI
C P10940;
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SPECIES=E.col; STRAIN=c157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Sasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Somplete genome sequence of enterchemorrhagic Escherichia coli O157:H7 and genome comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                          SPECIES E. COll; STRAIN=06:H1 / CFT073 / ATCC 700928;
MBDLINE=22389234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.,
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.",
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Zhao Z., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R., InDA sequence and analysis of 136 kilobases of the Escherichia coli genome: organizational symmetry around the origin of replication."; Genomics 16:S51-S61(1993).
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SPECIES=E.coli, STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Mesco D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkparrick H.A., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkparrick H.A., Grosfai G., Hackett J., Kink S., Boutin A., Shao Y., Miller L., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Meloh R.A., Blattner F.R., "Meloh R.A., Blattner F.R.,"
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.", Nature 409:529-533(2001).
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EMBL, M89480; AAA2743.1; ---
EMBL, AEG08876; AAA22648.1; --
PIR; P10957; 1A1853.
HSSP, P10957; 1RNL.
Stydene; SG10406; uhpA.
Interpro; IPR000799; RESPONSE_reg.
Pfam; PF00196; GerE; 1.
PRINTS; PR00039; HTHLUXR.
ProDom; PD000039; HTHLUXR.
ProDom; PD000039; HTHLUXR.
SWART; SW00421; HTH LUXR; 1.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00191; HIPH LUKR.
InterPro; IPR001792; HTH LUKR.
InterPro; IPR001792; HTH LUKR.
InterPro; IPR001792; HESPONSE_reg.
Pfam; PF001072; response_reg; 1.
PRINTS; PR000130; HTH_LUKR; 1.
PRODOM; PD000030; Response_reg; 1.
SWART; SW00421; HTH_LUKR; 1.
PROSITE; PS00422; HTH_LUKR; 1.
PROSITE; PS00422; HTH_LUKR; 1.
PROSITE; PS00422; HTH_LUKR FAMILY; 1.
PROSITE; PS00422; HTH_HUKR FAMILY; 1.
PROSITE; PS00422; HTH_HUKR; 1.
PROSITE; PS00422; HTH HUKR; 1.
PROSITE; PS00422; HTH
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28-FEB-2003 (Rel. 41, Last annotation update)
Transcriptional regulatory protein uhpA.
UHPA OR SYM3790.
Salmonalla typhimurium.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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                                                                                                                                                                                                                                                               EMEL; 110328; AAA62021.1; ---
EMEL; 110328; AAA62021.1; ---
EMEL; AE010444; AAC76692.1; ---
EMEL; AE0105598; AAG58868.1; ---
EMEL; AE010556; BAB38029.1; ---
EMEL; AE015386; AAA45232.1; ALT_INIT.
EMEL; AE015386; AAA45232.1; ALT_INIT.
EMEL; AE01591; AAP18964.1; ---
PIR; P91204; P91204.
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PA_SALTY STANDARD, PR
USP 5767;
01-MG-1992 (Rel. 23, Created)
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Matches
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Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica sercvar Typhimurium LT2.";
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                                                                                                                                                                                                                                                                         -!- FUNCTION: APPEARS TO BE THE POSITIVE ACTIVATOR OF UHPT TRANSCRIPTION.
-!- SUBCELLULAR LOCATION: CYLOPLASMIC (Probable).
-!- PTM: PHOSPHORYLATED BY UHPB (PROBABLE).
-!- SIMILARITY: COLTAINS 1 response requiatory domain.
-!- SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL REGULATORS.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBI_TaxID=10090;
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MEDLINE=99303612; PubMed=10373455;
Muramatsu M., Sankaranand V.S., Anant S., Sugai M., Kinoshita K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS5010; RESPONSE REGULATORY; 1.
PROSITE; PS50110; RESPONSE REGULATORY; 1.
Sensory transduction; Phosphorylation; Transcription regulation;
DNA-binding; Activator; Sugar transport; Complete proteome.
DOMAIN
MOD RES 54 54 PHOSPHORYLATION (BY SIMILARITY).
DNA BIND 155 174 H-T-H MOTIF (BY SIMILARITY).
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28-FEB-2003 (Rel. 41, Last sequence update)
Activation-induced cytidine deaminase (EC 3.5.4.5) (Cytidine aminohydrolase).
AICDA OR AID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 196;
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100.0%; Pred. No. 3.4e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 174 H-T-H MOTIF (BY SIMILARIT' 196 AA; 20790 MW; 4C80FF931C69078F CRC64;
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                                                                                           cells.";
J. Biol. Chem. 274:18470-18476(1999).

-!- FUNCTION: RNA-editing deaminase involved in somatic hypermutation, gene conversion, and class-switch recombination. Required for several crucial steps of B-cell terminal differentiation necessary for efficient antibody responses.

-!- CATALYTIC ACTIVITY: Cytidine + H(2)O = uridine + NH(3).

-!- COFACTOR: Zinc (By similarity).

-!- COFACTOR: Zinc (By similarity).
                          "Specific expression of activation-induced cytidine deaminase (AID), a novel member of the RNA-editing deaminase family in germinal center B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=AUCC 35092 / DSM 1617 / P2;
MEDLINE=20165948; PubMed=10701121;
Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,
Confalonieri F., Curtis B., Duguet M., Brauso G., Faguy D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
16-DEC-1998 (Rel. 41, Last annotation update)
18-FEB-2003 (Rel. 41, Last annotation update)
18-FEB-2013 (Rel. 41, Last annotation update)
18-FEB-2013 (Rel. 41, Last annotation update)
18-FEB-2013 (Rel. 18-FEB-2013)
18-FEB-
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
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SEQUENCE FROM N.A.
STRAIN=ARCC 35092 / DSM 1617 / P2;
MEDLINE=97352706; PubWed=9209067;
Charlebois R.L., Sensen C.W., Doolittle W.F., Brown J.R.;
"Evolutionary analysis of the hisCGABdFDEHI gene cluster from the archaeon Sulfolobus solfetaricus P2.";
J. Bacteriol. 179:4429-4432(1997).
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Pred. No. 3.5e+02;
0; Mismatches 0; Indels
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PROSITE; P800903; CYT DCMP DEAMINASES; 1.
PROSITE; P800903; CYT DCMP DEAMINASES; 1.
MRTAL S6 S6 ZINC (BY SIMILARITY).
MRTAL 87 87 ZINC (BY SIMILARITY).
MRTAL 90 90 ZINC (BY SIMILARITY).
CROUGENCE 198 A4; Z4030 MW; 18A3BA10CA54BEBZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF132979; AAD41793.1; -. MGD; MGI:1142279; Aicda. GO; GO:0004126; F:cytidine deaminase activity; IDA. InterPro; IPR007994; APOBEC C. InterPro; IPR02125; dCMP/cyt_deam.
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100.0%; Pred. No. 3.5e+
.... 0; Mismatches
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Best Local Similarity 1000.
Davidson N.O., Honjo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Kushwaha N., Lafleur B., Medina N., Peng X., Penny S.L., She Q., St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F., Ragan M.A., Sensen C.W.
                                               "Gene content and organization of a 281-kbp contig from the genome the extremely thermophilic archaeon, Sulfolobus solfataricus P2."; Genome 43:116-136 (2000).
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PIR, H90206, H90206.
HAMAP, MF 00218; -; I.
InterPro, IPR000991; GATase_1.
Pfam, PF00117; GATase; I.
PROSITE, PS00442; GATASE TYPE I; PALSE NEG.
Histidine biosynthesis, Transferase; Glutamine amidotransferase;
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RETH HORSE

AC Q28359,

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 38-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 17DB1A86724CE095 CRC64;
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100.0%; Pred. No. 3.5e+02;
ive 0; Mismatches 0;
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Hes 4; Conservative
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178
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ACT_SITE 76
ACT_SITE 178
ACT_SITE 180
SEQUENCE 199 AA;
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Best Local &
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retinol-binding protein.";
Nucleic Acids Res. 11:7769-7776(1983)
                                               SEQUENCE FROM N.A.
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                                                                                                          TISSUB-Endometrium;

MEDINE=95226610, PubMed=7536053;

MEDINE=95226610, PubMed=7536053;

MEDINE=95226610, Adams M.H., Franklin K.M., Baker C.B.;

MCDOwell K.J., Adams M.H., Franklin K.M., Baker C.B.;

McDowell K.J., Adams M.H., Franklin K.M., Baker C.B.;

Stockell K.J., Adams M.H., Pregnancy and with exogenous steroids.";

Biol. Reprod. 52:438-443(1995).

-I. FUNCTION: Delivers retinol from the liver stores to the peripheral tissues. In plasma, the RBP-retinol complex interacts with transchyretin, this prevents its loss by filtration through the kidney glomeruli.

-I. SUBCELDILAR LOCATION: Secreted.

-I. SUBCELDILAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
        Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-84069802; PubMed=6316270;
Colambuoni V., Romano V., Bensi G., Santoro C., Costanzo F.,
Raugei G., Cortese R.,
"Cloning and sequencing of a full length cDNA coding for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
Plaema; Vitamin A; Retinol-binding; Transport; Liver; Signal;
Lipocalin. 1 18 POTENTIAL.
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PLASMA RETINOL-BINDING PROTEIN
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 19; DB 1; Length 201; 100.0%; Pred. No. 3.5e+02; Live 0; Mismatches 0; Indels
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BY SIMILARITY.
12CF80834E4262DC CRC64;
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RETB HUMAN STANDARD; D8WWA3; Q9PL78; 21-JUL-1986 (Rel. 01, Created) 28-PBB-2003 (Rel. 41, Last sequence update) 28-PBB-2003 (Rel. 42, Last annotation update) 28-PBB-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U21208; AAC48461.1; -.
PIR; I46257; I46257.
HSSP; P27485; IAQB.
InterPro; IPR002345; Lipocalin.
InterPro; IPR00556; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; 1.
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201
178
192
147
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22
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88
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Best Local Similarity
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SEQUENCE FROM N.A.
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MEDLINE=2238827; PubMed=12477932;

A trausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A trausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A trausberg R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B tapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Asha S.S., McEwan P.J., McKernan K.J., Mar J.A., Gunaratne P. H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Rotteman M., Madan A., Rodriques S., Sanchez A.,

Butkerled Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Functional prediction of the coding sequences of 79 new genes deduced by analysis of cDNA clones from human fetal liver."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 18-201 FROM N.A.
TISSUE=Fetal liver;
Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structural and functional studies of vitamin A-binding proteins."; Ann. N.Y. Acad. Sci. 359:79-90(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-189 FROM N.A.

BDLINE=86655755; PubMed=298779;
D'Onofrio C., Colantuoni V., Cortese R.;
Structure and cell-specific expression of a cloned human retinol
"Structure and cell-specific expression of a cloned human retinol
specific gene: the 5'-flanking region contains hepatoma
specific transcriptional signals.";
EMBO J. 4:1981-1989 (1985).
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WEDLINE-88019004; PubMed-244402, Peterson P.A.;

Rask L., Anundi H., Follman J., Peterson P.A.;

"The complete amino acid sequence of human serum retinol-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 19-183.
MEDLINE=80004132; PubMed=573217;
Rask L., Anundi H., Peterson P.A.;
"The primary structure of the human retinol-binding protein.";
FEBS Lett. 104:55-58(1979).
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MEDLINE-81254137; PubMed=6942701;
Rask L., Anundi H., Boehme J., Eriksson U., Ronne H., Sege K.,
Peterson P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=91017498; Pubmed=2217163;
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MEDLINE=95395382; PubMed=7666002;
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Pfam; PR0061; lipocalin; 1.
PRINTS; PR00179; LIPOCALIN; 1.
PROSITE; PS00213; LIPOCALIN: 1.
PROSITE; PS00213; LIPOCALIN: 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Signal; Lipocalin; Disease mutation; Vision; 3D-structure.
                                                                                                                             GO; GO: 0005615; C:extracellular space; 1
GO; GO:0005501; F:retinoid binding; TAS.
InterPro; IPR002345; Lipocalin.
InterPro; IPR000566; Lipocalin_cytFABP.
PDB; 1BRP; 31-JAN-94.
PDB; 1BRQ; 31-JAN-94.
PDB; 1QAB; 09-APR-99.
SWISS-2DPAGE; P02753; HUMAN.
SIENA-2DPAGE; P02753; HUMAN.
GENEW; HGNC: 9922; RBP4.
MIM; 180250; -
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PRINGE=17-199.

DISEASE: Defects in RBP4 are a cause of retinol-binding protein deficiency [MIM:180250]. This condition causes night vision problems. It produces a typical "fundus xerophthalmicus," featuring a progressed atrophy of the retinal pigment epithelium.

Protein posttranslationally and results in defective delivery and protein posttranslationally and results in defective delivery and supply of vitamin to the epidermal cells (a condition associated with a dermatosis).

SIMILARITY: Belongs to the lipocalin family.

DATABARE: NAME=Mutations of the RBP4 gene;

NOTE=Retina International's Scientific Newsletter;

WWW="http://www.retina-international.com/sci-news/rlbp4mut.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [12]
VARIANTS RBP DEFICIENCY ASN-59 AND ASP-93.
VARIANTS PROPERSONAGE-9888420;
MEDLINES 99103495; PubMed-9888420;
Seeliger M.W., Bicanaki H.K., Wissinger B., Gollnick H., Gielen S., Frank J., Beck S., Zrenner E.;
Phenotype in retinol deficiency due to a hereditary defect in retinol binding protein synthesis.";

Dinding protein synthesis.";

Invest. Ophthalmol. Vis. Sci. 40:3-11(1999).
                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH TTR. MEDLINE=99162254; PubMed=10052934; Naylor H.M., Newcomer M.B.; "The structure of human retinol-binding protein (RBP) with its carrier protein transthyretin reveals an interaction with the carboxy terminus of RBP.";
         Owan S.W., Newcomer M.E., Jones T.A.; Crystallographic refinement of human serum retinol binding protein
                                                                                                                 MEDLINE=92322903; PubMed=1623143;
Monaco H.L., Zanotti G.;
"Three-dimensional structure and active site of three hydrophobic
molecule-binding proteins with significant amino acid sequence
       T.A.;
                                                                                                                                                                                                                                                                                                                                                             Biochemistry 38:2647-2653(1999)
                                                                                                                                                                                                           Biopolymers 32:457-465(1992).
                                                             Proteins 8:44-61(1990)
                                                                                                   X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                             similarity.";
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/FTId=VAR_009276. G -> D (in RBP deficiency). /FTId=VAR_009277. F -> L (IN REF. 1 AND 3). LGSGR -> WAA (IN REF. 1 AND 3).

-> N (in RBP deficiency)

201 178 192 147 59

138 138 59

PLASMA RETINOL-BINDING PROTEIN

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Trout W.B., MoDonnall J.J., Kramer K.K., Baumbach G.A., Roberts R.M.;
"The retinol-binding protein of the expanding pig blastccyst:
molecular cloning and expression in trophectoderm and embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-FAY CRYSTALLOGRAPHY (1.65 ANGSTROMS), AND REVISIONS TO 134 AND 185. MEDLINE=99437649; PubMed=9757135; Zanotti G., Panzalorto M., Marcato A., Malpeli G., Folli C., Berni R. "Structure of pig plasma retinol-binding protein at 1.65-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 1; Length 201
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
15-UTL-1998 (Rel. 36, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disc.";
Mol. Endocrinol. 5:1533-1540(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 VAEF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                      RETB_PIG
ID RETB_PIG
AC P27485;
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BC020633; AAH20633.1; -. X02775; CAA26553.1; -. X02824; CAB46489.1; -.

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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 18
19 201 PLL
22 178 BY
88 192 BY
138 147 BY
201 AA; 23102 MW;
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Best Local Similarity
'.aa 4; Conserv?
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=9986;
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YIGZ ECOLI
ID YIGZ ECOLI
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DISULFID
DISULFID
SEQUENCE
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                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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resolution.";
Acta Crystallogr. D 54:1049-1052(1998).
-!- FUNCTION: Delivers retinol from the liver stores to the peripheral
-!- FUNCTION: In plasma, the RBP-retinol complex interacts with
tissues. In plasma, the RBP-retinol complex interacts with
transthyretin, this prevents its loss by filtration through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 PER, A39466; AAA31113.1; -; PER; A39466; AAA3113.1; -; PER; A39466; A39466; A39466; A39466; A39466; A39466; A39466; A19002345; Lipocalin.
InterPro; IPR0002545; Lipocalin.
PROSITE; PR000121; Lipocalin; 1.
PROSITE; PR000121; Lipocalin; 1.
PROSITE; PR00131; LIPOCALIN; 1.
PR0131; LIPOCALIN; PR0131; LIPOCAN; PR0131; LIPOCAN;
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                                                                                                     Liminsurversity kidney glomeruli.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the lipocalin family.
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THE RABIT STANDARD;
PO6512;
01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M68860; AAA31113.1; -.
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Best Local Similarity
Matches 4; Conserv
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PSECURATE OF 19-201.

NEDLINE-85207643; PubMed=1838985;

NEDLINE-85207643; PubMed=1838985;

NEDLINE-85207643; PubMed=1838985;

NEDLINE-85207643; PubMed=1838985;

A Bjoerck L., Eriksson U., Aakerstroem B., Jones A., Newcomer M.,

Rash L., Rask L.;

Rash L., Rask L.;

Rash L., Rask L.;

Rash L., Aakerstroem B., Jones A., Newcomer M.,

RT Anino acid sequence homologies between rabbit, rat, and human serum

RT Anino acid sequence homologies between rabbit, rat, and human serum

RT Treinol-binding proteins:

CC -: FUNCTION: Delivers retinol from the liver stores to the peripheral

CC -: FUNCTION: Delivers retinol from the liver stores with

CC transtyretini, this prevents its loss by filtration through the

Ridney glomeruli.

CC -: SUBCELULAR LOCATION: Secreted.

CC -: SUBCELULAR LOCATION: Secreted.

CC -: SUBLINIARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is nor as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteléostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 845958; AAB23582.1; -.
PIR; A49178; VARB.
HSSP; P18902; 1PRN.
InterPro; IPRN02345; Lipocalin.
InterPro; IPRN00346; Lipocalin.
PFAM; PF00061; lipocalin; 1.
PRINTS; PR00179; LIPOCALIN; 1.
PROSITE; P8001213; LIPOCALIN; 1.
PROSITE; P8001213; LIPOCALIN; 1.
PROSITE; P8001214; LIPOCALIN; 1.
PROSITE; P8001214; LIPOCALIN; 1.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
4153FCF050184136 CRC64;
                                                                                                                                                                              MEDLINE-93011736; PubMed-1339354;
Lee S.Y., Ubels J.L., Soprano D.R.;
"The lacrimal gland synthesizes retinol-binding protein.";
Exp. Eye Res. 55:163-171(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Length 201;
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01-AUG-1992 (Rel. 23, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mypothetical protein yigz.
XIGZ OR B3848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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201 AA.

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Luo X., Far
Wagner G.,
GCCCCCCTRICER SERVICE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94147996; Pubmed=8313894; Koomin B.V., Bork P., Sander C.; "Yeast chromosome III. new gene functions."; EMBO J. 13:493-503(1994).
                                                                                            [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SECRAIN-KI2 / MG1655;
MEDLINE=92358234; PubMed=1379743;
Daniels D.L.; Plunkett G. III, Burland V.D., Blattner F.R.;
Daniels D.E.; Plunkett G. III, Burland V.D., Blattner F.R.;
Manalysis of the Escherichia coli genome: DNA sequence of the region from 84:5 to 86.5 minutes.";
Science 257:771-778(1992).
[2] SEQUENCE FROM N.A.
STRAIN-KLS;
STRAIN-KLS;
STRAIN-KLS;
STRAIN-KLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Nucleotida esquence between the fadB gene and the rrnA operon from
Escherichia coli.";
Escherichia coli.
Bacteriai, Frotecobacteria, Gammaprotecobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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204 AA; 21757 MW; 97E48163FE899DBE CRC64;
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100.0%; Pred. No. 3.6e+02;
iive 0; Mismatches 0;
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 18:6439-6439(1990).
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EMBL, AE000460, AAC76851.1, ALT INIT.
EMBL, X54687, CAA38501.1, ALT INIT.
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InterPro, IPR009022, EFG III_V.
InterPro, IPR001498, UPF0029.
IEMI, PF01205, UPF0029, I.
TIGRPAMS, TIGR00257, TIGR00257, I.
PROSITE, PS00910, UPF0029, I.
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91057145; PubMed=2243799;
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Best Local Similarity 100.
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                                                                           NCBI_TaxID=562;
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D21_HUMAN
D_MD21_HUMAN
.C_Q13257;
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TISSUE=Bone marrow, and Muscle;

WEDLINE=22388557; Pubmed=12477932;

REDLINE=22388557; Pubmed=12477932;

Strausberg R.L., Colling F.G., Wagner L., Shemmen C.M., Schuler G.D.,

Riaugner R.D., Colling F.G., Wagner L., Shemmen C.M., Schuler G.D.,

A lischul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Baba N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Manny J., Hsieh F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Expleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garrinci P., Prange C.T.,

Raha S.A., McKernan N.J., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Morley K.C., Hale S., Garria A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodfigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butcerfield Y.S.N., Krzywinski M.L., Skalska U., Smallus D.E.,

"Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences",

"Generation and initial analysis of more than 15,000 full-length
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Nat. Struct. Biol. 7:224-229(2000).
-I. FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND DELAYS THE CONST OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLETE. IT SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE METAPHASE PLATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99458664; PubMed-10527948;
Nelson K.K., Schlondorff J., Blobel C.P.;
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"Evidence for an interaction of the metalloprotease-disintegrin tumour necrosis factor alpha convertase (TACE) with mitotic arrest deficient 2 (NAD2), and of the metalloprotease-disintegrin MDC9 with a novel MAD2-related protein, MAD2-beta.";
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"The checkpoint protein MAD2 and the mitotic regulator CDC20 fc
ternary complex with the anaphase-promoting complex to control
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Luo X., Fang G., Coldiron M., Lin Y., Yu H., Kirschner M.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nobori T.;
Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  Jin D.-Y., Jeang K.-T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases
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MEDLINE=20165182; PubMed=10700282;
[1]
SEQUENCE FROM N.A.
MEDLINE=96421709; PubMed=8824189;
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SEQUENCE FROM N.A.

STRAIN=129;
MEDILINE=20348739; PubMed=10892650;
Dobles M., Liberal V., Scott M.L., Benezra R., Sorger P.K.;
Chromosome missegregation and apoptosis in mice lacking the mitotic checkpoint protein Mad2.";
Cell 101:635-642000).
-!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT Cell 101:635-642000.
-!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT CHICK MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND DELAYS THE ONSET OF ANAPHASE PROMOTING COMPLETE. IT CHAPPASE PLATE (BY SIMILARITY).

SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE METAPRASE PLATE (BY SIMILARITY).
--- SUBDMIT: INTERACTS WITH CDC20.
--- SUBDMIT: INTERACTS WITH CDC20.
--- SUBDMIT: SELONGS TO THE MAD2 FAMILY.
--- SIMILARITY: CORTAINS IN HORMA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
   MAD21.1 OR MAD2A.
Mus musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                   [1] SEQUENCE FROM N.A. STRAINS TISSUE-Embryo; STRAINS-C57EL/6J; TISSUE-Embryo; STRAIND.-Y. Jeang X.-T.; Identification of a novel component of the spindle assembly checkpoint in mammalian cells."; submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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R HSSP; Q123.7; LDUJ.
R MGD; MG71860374; Mad211.
R MGO; GO:0000776; C:kinetochore; IDA.
R GO; GO:0000776; C:kinetochore; IDA.
R GO; GO:0000709; P:mitotic chromosome segregation; IMP.
R GO; GO:0007094; P:mitotic chromosome segregation; IMP.
R GO; GO:007094; P:mitotic chromosome segregation; IMP.
R GO; GO:007094; P:mitotic chromosome segregation; IMP.
R GO; GO:007094; P:mitotic chromosome segregation; IMP.
R Ffam; PF02301; HORMA; 1.
R PROSITE; PS50815; HORMA; 1.
Cell cycle; Mitosie; HORMA; 1.
DOMAIN.
14 197 HORMA.
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178 C -> S (IN REF. 1).
201 T -> I (IN REF. 1).
23558 MW, A9F3F28BC4C9738E CRC64;
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
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-i- SUBUNIT: INIBARALLO

-i- SUBCELLULAR LOCATION: Nuclear.

-i- SIMILARITY: BELONGS TO THE MAD2 FAMILY.

-i- SIMILARITY: Contains 1 HORVA domain.

-i- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;

-i- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;

-i- DATABASE: NAME-Atlas Genet. Tytogenet. Oncol. Haematol.;

-i- DATABASE: NAME-Atlas Genet. Tytogenet. Oncol. Haematol.;

-i- Tris produced through a collaboration.
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21 MOUSE
PR21 AD MOUSE STANDARD; PRT; 205 AA.

QP21B5; Q9J153;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2003 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last samotation update)
Mitotic spindle assembly checkpoint protein MAD2-like 1).
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EMBL; AJ00186; CAA03343.1; -
EMBL; AD056160; BAB63410.1; -
EMBL; BC000356; AAH05056.1; -
EMBL; BC000356; AAH050356.1; -
EMBL; BC005345; AAH05045.1; -
EMBL; BC005345; AAH05045.1; -
EMBL; BC005045; AMAD201.

GK; Q13257; --
MIN; 601467; -
GQ; GO:0005699; C:kinetochore; TAS.
GQ; GG:0007067; P:mitcais; TAS.
GQ; GO:0007067; P:mitcais; TAS.
GQ; GO:0007067; P:mitcais; TAS.
GQ; GO:0007067; P:mitcais; TAS.
GQ; GO:0007067; P:mitcais; TAS.
GQ; GG:0007067; P:mitcais; TAS.
GQ; GG:0007067; P:mitcais; TAS.
GG: GG: GG: FRR003511; DNAbind_HORWA.
FRAm; PF02301; HORWA; 1.
FROSTE; PSS0815; HORWA; 1.
FROSTE; PSS0815; Mitcais; Nuclear protein; 3D-structure.
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39 VAEF 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                          STRAIN=Philadelphia 1;
MEDUINE=93374664; PubMed=8366052;
MEDUINE=93374664; PubMed=8366052;
Mengaud J.M., Horwitz M.A.;
Mengaud J.M., Horwitz M.A.;
"The major iron-containing protein of Legionella pneumophila is an aconitase homologous with the human iron-responsive element-binding
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STATN=Blockype grave, NCTC 13129;

STATN=Blockype grave, NCTC 13129;

A MEDLINE=2296543; PubMed=4602910;

Cerdeno-Tarraga A.M., Efstratiou A., Dover L.G., Holden M.T.G.,

A Pallen M., Bentley S.D., Besra G.S., Churcher C., James K.D.,

De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,

A Hamlin N., Holroyd S., Jagels K., Moule S., Quall M.A.,

A Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,

Mitchead S., Barrell B.G., Parkhill J.;

A Whitchead S., Barrell B.G., Parkhill J.;

A Mitchead S., Barrell B.G., Parkhill J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                   Legionella pneumophila.
Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales,
Legionellaceae, Legionella.
NCBI_TaxID=446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacceria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 1; Length 208; 100.0%; Pred. No. 3.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A48642; A48642.
Hypothetical protein.
SEQUENCE 208 AA; 23714 MW; IESC75E63A20C800 CRC64;
Hypothetical 23.7 kDa protein in acn 5'region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Heme oxygenase (EC 1.14.99.3).
HAWOOR DIP1669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 AA.
                                                                                                                                                                                                                      protein.";
J. Bacteriol. 175:5666-5676(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97158681; PubMed=9006041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hemoglobin.";
J. Bacteriol. 179:838-845(1997),
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L22081; AAA25294.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 VAEF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HMUO COR
P71119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UOUHHHWXWUUXXBUXXBUXXBEHHHYXBUXXXXXXXX
   M W O O X X A O X 4 F F F J O O O O O O O O
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                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINES 96050477 FubMed=7561763;

MEDLINES 96050477 FubMed=7561763;

MCGarvey P.B., Tousignant M., Geletka L., Cellini F., Kaper J.M.;

MCGarvey P.B., Tousignant M., Geletka L., Cellini F., Kaper J.M.;

"The complete sequence of a cucumber mosaic virus from Ixora that is deficient in the replication of satellite RNAs.";

Gef. Cont. Virol. 76:2257-2270 (1995).

-: SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

E -> K (IN REF. 1).

A -> V (IN REF. 1).

A -> GS (IN REF. 1).

N -> H (IN REF. 1).
-i- FUNCTION: Allows the bacteria to use the host heme as an iron source. Involved in the oxidation of heme and subsequent release of iron from the heme moiety.
-i- CATALYTIC ACTIVITY: Heme + 3 AH(2) + 0(2) = biliverdin + Fe(2+) + CO + 3 A + 3 H(2)0.
-i- SIMILARITY: Belongs to the heme oxygenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coat protein (Capaid protein) (CP).
Cucumber mosaic virus (strain Ixora) (CMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 1; Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60D9E8E2ED7ED456 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, UZ0219; AAC54619.1; -.
PIR, D71392; D71392; D71392.
INCEPTO; IRR002347; Cucumovirus coat.
INCEPTO; IPR008975; Viral_cap_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfan; PP01126; Heme oxygenase; 1.
PRINTS; PR00088; HAEMOXYGNASE.
PROSITE; PS00593; HEME_OXYGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                        EMBL; U73860; AAC44832.1; -.
EMBL; BXX48358; CAE50198.1; -.
HASSP; P09601; 1008.
InterPro; IPR002051; Heme_oxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 IEC
34 E E
60 A
93 DG
192 N
24116 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heme; Oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
34
60
92
192
1192
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SULT 65

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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable exosome complex RNA-binding protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001070; AAB90745.1; -. PIR; D69311; D69311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                   Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 VAEF 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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RAN_TETPY
      BUT THE SOURCE COURT THE SECOND SECON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BKME outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The sequence of the Orgyia pseudotsugata multimucleocapsid nuclear polyhedrosis virus genome."; Virology 227:381-399(1997).
-!- CAPALYTION: COULD BE INACTIVE AS THE ACTIVE SITE CYSTEINE IS MODIFIED TO TRYPTOPHAN.
-!- CAPALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate + phosphate TY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY: CDC14 SUBFAMILY.
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                   .,
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

BLILINE-27213100; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUIVALENT OF ACTIVE SITE CYS. D3FC093F1953D425 CRC64;
                                                                                                                                                                      95.0%; Score 19; DB 1; Length 218; 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 220; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels
                                                                                                               218 AA; 24185 MW; 130E82D17BD75224 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Putative protein-tyrosine phosphatase 1 (EC 3.1.3.48).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000387; TYR phosphatase.
PROSITE; PS00383; TYR PHOSPHATASE 1; FALSE NEG.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 AA
Pfam; PF00760; Cucumo coat; 1.
PRINTS; PR00222; CUCUMOCOAT.
ProDom; PD001284; Cucumovirus_coat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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SEQUENCE 220 AA; 25234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULT 66
R1 ARCFU
CSCR1 ARCFU STANDARD;
10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U75930; AAC59009.1; -.
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Best Local Similarity 100...
And 4, Conservative
                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 VÀÈF 142
                                                                                                                                                                                                                                                                                                                                      96 VAEF 99
                                                                                                                                                                                                                                                                                      2 VAEF 5
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                                                                                    Coat protein.
SEQUENCE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                         P1_NPVOP
PTP1_NPVOP
O10274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase.
SITE
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                                                                                                                                                                         STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MEDLINES-886494313; PubMed=9389475;

Klenk H.-P., Clayton R.A. Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerladavage A.R., Graham D.E., Kyrpides N.C.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Korbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.C., Woose C.R.,

Wenter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: Component of the archaeal exosome multienzyme ribonuclease complex (Potential).
-1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-1- SIMILARITY: Contains 1 KH domain.
-1- SIMILARITY: Contains 1 S1 motif domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 223; 100.0%; Pred. No. 3.9e+02; artive 0; Mismatches 0; Indels
Archaeea; Euryarcheeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 223 AA; 24725 MW; A11B7F1A26972833 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50084; KH TYPE 1; 1.
PROSITE; PS50126; S1; 1.
Exosome; RNA-binding; Complete proteome.
DOMAIN 135 127 KH.
FINALN 135 193 KH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGE, AF0492;

TIGE, AF0492;

INTERON, MF 00623;

INTERPO, IPR004089; KH Lype_1.

INTERPO: IPR008994; NuCleic_acid_0B.

INTERPO: IPR008994; NuCleic_acid_0B.

PEam; PF00513; KH; 1.

SWART; SM00325; K1; 1.

SWART; SM00316; S1; 1.
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Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
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nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=B1868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 VAEP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VAEF 5
                                                   NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                       (+) (Out)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAN TETTH
P41915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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RAN TETTH
δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBCNIT: Monomer.
-:- SUBCELTULAR LOCATION: Nuclear (By similarity).
-:- SUBCELTULAR LOCATION: Nuclear (By similarity).
-:- SIMILARITY: Belongs to the small GTPase superfamily. Ran family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 144:123-125(1994).
-!- FUNCTION: GTP-binding protein involved in nucleocytoplasmic transport. Required for the import of protein into the nucleus and also for RNA export. Involved in chromatin condensation and control of cell cycle (By similarity).
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16-OCT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
V-type ATP synthase subunit D (EC 3.6.3.14) (V-type ATPase subunit D).
Thermus thermophilus.
                                                                                                                         GTP-binding nuclear protein RAN/TC4.
Tetrahymena pyriformis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                     STRAIN=W;
MEDILINE=94299154; PubMed=8026746;
MEDILINE=94299154; PubMed=8026746;
Nogata K.-I., Takemasa T., Alam S., Hattori T., Watanabe Y.,
Nozawa Y.;
Nozawa Y.;
"Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding
low-M(r) (GBLM) protein, Ran/TC4, from micronucleated Tetrahymena
thermophila and amicronucleated Tetrahymena pyriformis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r protein, Protein transport.
25 GTP (BY SIMILARITY).
70 GTP (BY SIMILARITY).
126 GTP (BY SIMILARITY).
143 IBB (BY SIMILARITY).
25422 NW, 5474DADB5ABF0977 CRC64;
                                                (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P17080; 1A2K;
InterPro; IPR002041; RAN.
InterPro; IPR0010806; Rag trinsfrung.
InterPro; IPR0010806; Rag trinsfrung.
InterPro; IPR005225; Small_GTP.
Pf.M. PR0057; Small_GTP.
PRINTS; PR00642; GTPRANTC4.
PRINTS; PR00449; RASTRNSFRWNG.
SWART; SW00116; RAN; 1.
INGREAMS; TIGR00231; small_GTP; 1.
PR05ITE; PS01115; RAN; 1.
PR0FIND 18 25 GTP (BY SN PEND) 12 GTP (BY SN PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D21825; BAA04849.1; -. HSSP; P17080; 1A2K.
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  STANDARD;
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223 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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RAN TETPY
P41914;
01-NOV-1995 (
                                                                                                        28-FEB-2003
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D_VATD_THE
C_087880;
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"Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding
"Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding
low-M(r) (GELM) protein, Ran/TC4, from micronucleated Tetrahymena
thermophila and amicronucleated Tetrahymena pyriformis.";
Gene 144:123-125(1994)
-!- FUNCTION: GTP-binding protein involved in nucleocytoplasmic
- FUNCTION: Required for the import of protein into the nucleus and
also for RNA export. Involved in chromatin condensation and
control of cell cycle (By similarity).
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
GTP-binding nuclear protein RAN/TC4.
Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the small GTPase superfamily. Ran family.
                                                                                                                 Yokoyama K., Ohkuma S., Taguchi H., Yasunaga T., Wakabayashi T., Yoshida M.;
Yoshida M.;
Yoshida M.;
Yoryoe H.A.TPasse/synthase from a thermophilic eubacterium, Thermus thermophilus. Subunit Erructure and operon.";
J. Biol. Chem. 275:13955-13961(2000).
-!-FUNCTION: Prociduces ATP from ADP in the presence of a proton
                                                                                                                                                                                                                                                                                                                                                                              gradient across the membrane. 
 -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 1; Length 223; 100.0%; Pred. No. 3.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the V-ATPase D subunit family.
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Prodom; PD004122; ATPsynt_Dsub; 1.
TIGRAMS; TIGR00309; V. ATPsace subb; 1.
Hydrolase; ATP synthesis; Hydrogen ion transport.
SEQUENCE 223 AA; 24677 WW; B666AE00DFE0B08B CRC64;
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SEQUENCE FROM N.A.
STRAIN=HB8 / ATCC 27634;
MEDLINE=20250964; PubMed=10788522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MF_00271; -; 1.
ro; IPR002699; ATPsynt_Dsub.
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EMBL; I
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                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDINTE-89293088; PubMed=2661722;
MEDINTE-89293088; PubMed=2661722;
Gombart A.F., Blisard G.W., Rohrmann G.F.;
"Characterization of the genetic organization of the HindIII M region of the multicapaid nuclear polyhedrosis virus of Orgyia pseudotsugata reveals major difference among baculoviruses.";
J. Gen. Virol, 70:1815-1828(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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01-MAR-1992 (Rel. 21, Last sequence update)
01-MOV-1997 (Rel. 31, Last annotation update)
11-MOV-1997 (Rel. 35, Last annotation update)
01-MOV-1997 (Rel. 36, Max protein in PP34-EXO intergenic region (ORF 4).
01cgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses, dsDNA viruses, no RNA stage, Baculoviridae,
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Virology 229:881-399(1997).
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MEDLINES97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; r. PRO062, PRSTRNS. PRINTS; PRO0449; RASTRNS. PRINTS; PRO0449; RAN; 1.
TIGRRAMS; TIGRO231; small_GTP; 1.
PROSITE; PSO1115; RAN; 1.
GTP-binding; Nuclear protein; Protein transport. GTP-binding; Nuclear protein; PS SIMILARITY).
18 (SY SIMILARITY).
19 (GTP (BY SIMILARITY).
19 (GTP (BY SIMILARITY).
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100.0%; Pred. No. 3.9e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                  INCEMPIC; IPRO02041; RAN.
INTERPIC; IPR001806; Ras trnsfrmug.
INCEMPIC; IPR00525; Small_GTP.
PRIMTS; PR00627; GTPRANTC4.
PRINTS; PR00449; RASTRNSFRMNG.
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Les 4; Conservative
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) Y132 NPVOP
P24080;
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InterPro; IPR004800; Cytidylyltransf.
Pfam; PF01467; CTP transf_2; 1.
Pyridine nucleotide blosynthesis; Transferase; Nucleotidyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metabolically versatile Pseudomonas putida KT2440.";
Environ. Microbiol. 4:799-808(2002).
-!- FUNCTION: Catalyzes the reversible adenylation of nicotinate
monouclectide (NaNN) to nicotinic acid adenine dinucleotide
(NaAN) (By similarity).
-!- CATALYTIC ACTIVITY: ATP + nicotinate ribonucleotide = diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple B., Scanlan D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (RC 2.7.7.18)
10-OCT-2003 (Rel. 42, Last annotation adenylyltransferase) (NaMN)
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0
                                                                                                                                                                                                                                                        Length 228;
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                                                                                                                                                 .l protein, Late protein.
228 AA; 25962 MW; F0766AD21F60039D CRC64;
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4e+02;
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-!- PATHWAY: NAD biosynthesis.
-!- SIMILARITY: Belongs to the nadD family.
                                                                                                                                                                                                                                                 95.0%; Score 19; DB 100.0%; Pred. No. 4e+:ive 0; Mismatches
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MEDLINE=22423060; PubMed=12534463;
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D13796; BAA02952.1; -. D13929; BAA03030.1; -. U75930; AAC59129.1; -.
                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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SEQUENCE 230 AA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adenylyltransferase).
NADD OR PP4810.
                                                                                                       PIR; D30857; D30857
Hypothetical protein
SEQUENCE 228 AA;
                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 VAEF 87
                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADD PSEPK
                                                                                                                                                                                                                                                            Query Match
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us-09-594-978a-3.rsp

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UBIE CORGL
QBNT39;
UBIE COREF
QBFSB3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 74
UBIE_CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 30S ribosomal protein S3.
RPS3.
Porphysa purpurea.
Chloroplast.
Chloroplast.
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
NCBI_TaxID=2787;
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Avonport;
Reith M.E., Munholland J.;
"Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome.";
plant wol. Biol. Rep. 13:333-335 (1995).
-!- SUBUNT: Part of the 30S ribosomal subunit.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SUBCELLULAR belongs to the S3P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
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Query Match 95.0%; Score 19; DB 1; Length 230; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00417; Ribosomal_S3_N; 1.
SMART; SM00322; KH; 1.
TIGRFAMS; TIGR01009; PEGC_bact; 1.
PROSITE; PS00548; RIBOSOMĀL_S3; 1.
PROSITE; PS00548; RIBOSOMĀL_S3; 1.
PROSITE; PS00548; RIBOSOMĀL_S3; 1.
PROSITE; PS00548; RIBOSOMĀL_S3; 1.
SEQUENCE 230 AB; 25631 MW; 5489B93704D7F0ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 1; Length 230; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMMP; MF 01309; -: 1.
InterPro; PR004097; KH dom.
InterPro; IPR004097; KH dom.
InterPro; IPR004044; KH TVPE Z.
InterPro; IPR001351; Ribosomal_S3_C.
InterPro; IPR00882; Ribosomal_S3_N.
InterPro; IPR008082; Ribosomal_S3_N.
Pfam; PF00113; KH; 1.
Pfam; PF00119; Ribosomal_S3_C; I.
Pfam; PF00119; Ribosomal_S3_C; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U38804; AAC08194.1; -. PIR; 873229; 873229.
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Query Match
Best Local Similarity 100.vv
Bernan 4; Conservative
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 VAEF 121
                                                                                                     42 VAEF 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Methyltransferase required for the conversion of dimethylmenaquinone (DMKH2) to menaquinone (MKH2) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens."; Genome Res. 13:1572-1579(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Menaquinone biosynthesis methyltransferase ubis (EC 2.1.1.-).
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; Pubmed=12840036;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.;
                                                     10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Menaquinone biosynthesis methyltransferase ubis (BC 2.1.1:-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterineae; Corynebacterium.
                                                                                                                                                                                              Corynebacterium efficiens.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 1; Length 230; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAWAP, MF_01813, -; 1.
InterPro; IPR001601; Methyltransf.
InterPro; IPR004051; ASM bind.
InterPro; IPR004033; UbiE/COO5 Metrf.
Pfam; PF01209; Ubie methyltran; 1.
PROSITE; PS01183; UBIE_1; PALSE_NEG.
PROSITE; PS01184; UBIE_2; PALSE_NEG.
Menaquinone biosynthesis; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 AA; 25366 MW; E10DCB602A1CD886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s-adenosyl-L-homocysteine + menaquinol.
-!- PATHWAY: Menaquinone biosynthesis; last step.
-!- SIMILARITY: Belongs to the ubiE family.
230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP005215; BAC17291.1; ALT_INIT.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
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STANDARD;
                                                                                                                                                                                                                                                                                NCBI_TaxID=152794;
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SEQUENCE FROM N.A.
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SEQUENCE 230 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                "Complete grounic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MNY-2002) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Methyltransferase required for the conversion of
dimethylmenaquinone (DMKH2) to menaquinone (MKH2) (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol =
-s-adenosyl-L-homocysteine + menaquinol.
-!- PATHWAY: Menaquinone biosynthesis; last step.
-!- SIMILARITY: Belongs to the ubiE family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=E.col1;
MEDLINE=92223101; PubMed=1314093;
Yang T.-P., Depew R.E.;
"Nucleotide sequence of a region duplicated in Escherichia coli toc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-KI2 / MG1655; SPECIRES-E.coli; STRAIN-KI2 / MG1655; MEDIJNES-97426617; PubMed-9278603; Blattner F.R., Flunkett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Flunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shoo Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.0%; Score 19; DB 1; Length 230; Sest Local Similarity 100.0%; Pred. No. 4e+02; Atches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01209; Ubie methyltran; 1.
PROSITE; PS01103; UBIE 1; FALSE NEG.
PROSITE; PS01184; UBIE 2; FALSE NEG.
Menaquinone blosynthesis; Transferse; Methyltransferse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 AA; 25244 MW; A8548173B7901400 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein yglB.
YGBL OR B3037 OR C3783 OR SF3077 OR S3282.
Escherichia coli,
Escherichia coli O6, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutants.";
Biochim. Biophys. Acta 1130:227-228(1992)
                                                                                                                                                                                                                                                                                                                                                                                                         HAMAR, MF 01813; -; 1.
InterPro; IPR001601; Methyltransf.
InterPro; IPR000051; SAM bind.
InterPro; IPR004033; UblE/COO5_Metrf.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP005275; BAB97864.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 VAEF 148
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IB ECOLI
YGIB ECOLI
P24195;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=2288224; PubMed=12471157;
Melch R.A., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yu J;
"Genore sequence of Shigella flexneri 2a: insights into pathogenicity
through comparison with genomes of Escherichia coli K12 and O157.";
Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Bcodene; EG11164; ygila
Hypcthetical protein; Complete proteome.
SEQUENCE 234 AA; 24868 MW; 08D5DE931072C966 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AE000385, AAC76073.1; -.
EMBL, AE016766, AAM82227.1; -.
EMBL, AE015319; AAM44555.1; ALT_INIT.
EMBL, AE016988; AAP18368.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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GenCore version 5.1.6
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protein - protein search, using sw model

1 on:

May 24, 2004, 17:33:08 ; Search time 35.7143 Seconds (without alignments) 44.173 Million cell updates/sec

US-09-594-978A-3

20 1 XVAEF 5 :le: rfect score: inence: BLOSUM62 Gapop 10.0 , Gapext 0.5 oring table:

1017041 tal number of hits satisfying chosen parameters: 1017041 segs, 315518202 residues arched:

nimum DB seq length: 0 ximum DB seq length: 2000000000

st-processing: Minimum Match 0% Maximum Match 100% Listing first 1000 summaries

SPTREMBL_25:*

1: Sp archea:*
2: Sp bacteria:*
3: Sp_fungi:*
4: Sp_human:*
1: Sp_mammal:*
5: Sp_mammal:*
5: Sp_mammal:*
5: Sp_mammal:*
5: Sp_mammal:*
5: Sp_mammal:*
5: Sp_phage:*
5: Sp_phage:*
5: Sp_phage:*
5: Sp_phage:*
5: Sp_organelle:*
5: Sp_o sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_rvirus:* sp_bacteriap:* sp_archeap:* tabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q7zx07 xenopus lae Q8u746 agrobacteri Q8pgn2 xanthomonas Q8zzc4 pyrobaculum Q18z7 Genorhabdi Q8erv9 encephalito Q9lnr7 arabidopsis Q8vgpl mus musculu Q3cpd4 streptomyce Q8vgg8 mus musculu Q9chG2 lactococcus Q8n114 corynebacte Q7v947 prochloroco	Q9+000 arabidopsis Q84948 mus musculu Q7trc3 mus musculu Q98re1 mycoplasma Q8py5 methanosarc Q9x6e6 homo sapien Q9zec1 lycopersico Q9gp66 arabidopsis Q8429 oryza sativ Q8420 mus musculu Q9mq9 amsacta moo Q9ck67 pasteurella	Q12125 saccharomyc Q7xty9 oryza sativ Q8nqr2 ocrynebacte Q25701 plasmodium Q25x69 thizobium Q25x69 thizobium m Q92x6 listeria in Q8y6k0 listeria an Q7u8g9 synechococc Q8wqx2 leishmania Q8vfd7 mus musculu Q7try1 mus musculu Q8yk1 anabaena sp Q8ybb2 xanthomonas Q8ybb2 xanthomonas Q8ybb2 xanthomonas Q8byb2 xanthomonas Q8trob9 homo sapien Q9tu97 pan troglod Q9tu87 gorilla gor Q9tu87 gorilla gor Q9tu80 gorilla go
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Q9R5C0 PRELIMINARY; PRT; Q9R5C0; C1-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last seq 01-UTM-2000 (TrEMBLrel. 14, Last ann Cytochrome P-460 (Fragment).
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O3168 arachaeoglob
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Q81409 mus musculu
Q82600 escherichia
Q8141 methanosarc
Q8461 methanosarc
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Q8645 drosophila
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Q8148 arabidopsis
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Q8n6a0 homo sapien
Q7wx56 alcaligenes
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytotoxin-binding protein (Fragment).
Cytotozin-binding protein (Fragment).
Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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MEDLINE=94039134; PubMed=7693466;
Lutz F., Mohr M., Grimmig M., Leidolf R., Linder D.;
Lutz F., Mohr M., Grimmig M., Leidolf R., Linder D.;
"Pseudomonas aeruginosa cytotoxin-binding protein in rabbit erythrocyte membranes. An oligomer of 28 kDa with similarity to transmembrane channel proteins.";
Eur. J. Biochem. 217:1123-1128 (1993).
PIR; $39049; $39049.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000425; MIP.
Pfam; PF00230; MIP; 1.
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                                                                   Q812Y4
O30168
Q9XSF7
Q83UD0
Q7WZ93
Q854X2
Q8LAG7
P97827
Q9Z2J2
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Q8ECB9
Q8ECB9
Q8ECG9
Q8FEC9
Q8T711
Q8T714
Q9CCZ8
Q9ST72
Q9ST73
Q9ECG
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Q9CAH5
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin regulatory light chain 2 (MLC-2) (Fragment).
Bombyx mori (Silk moth).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
NCBI_TaxIb=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93224468; PubMed=8385668; MEDLINE=93224468; PubMed=8385668; MCTavish H., LaQuier F., Arciero D., Logan M., Mundfrom G., McTavish H., LaQuier F., Arciero D., Logan M., Mundfrom G., Multiple copies of genes coding for electron transport proteins in the bacterium Nitrosomonas europaea."; J. Bacterium Nitrosomonas europaea."; J. Bacteriul. 175:2445-2447(1993).
SEQUENCE 22 AA; 2549 MW; C22664F5EBICE75F CRC64;
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MEDIANE=21177481; PubMed=11280994;
Zhong B.X.;
"Protein database for several tissues derived from five instar of
                                                                                                                                                                                                                                                                    Cytochrome P-460 (Fragment, .
Nitrosomonas europaea.
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
NGH _TaxID=915;
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Pred. No. 4.7e+02;
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SEQUENCE
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Q9TQR7
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Q48420
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MEDLINE=9739467; PubMed=9252185;
MEDLINE=9739467; PubMed=9252185;
Tomb U.F., White O., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Neleson K., Quackenbush U., Zhou L., Kirkness B.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Bergo D.E., Gocayne U.D., Utterback T.R., Peterson J.D., Kelley J.M., Gotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
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   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the gastric pathogen Helicobacter pylori.";

Mature 318-47 (1997).

EMBL; AE000596; AAD0'920.1; -.

PIR; G64625; G64625.

TIGR; HP9047; -.

Hypothetical protein; Complete proteome.

SEQUENCE 33 AA, 3704 MW; FA3F52631C0DB943 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=IN2 / ATCC 51768 / DSW 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
Miller J.H.;
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   Indels
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Archaea; Crenarchaecta; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                025518;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein HP0847.
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Mismatches
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4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                              13 VAEF 16
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01-MAR-2002 (
01-JUN-2003 (
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048420;
048420;
01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 25, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
14. Prothetical protein (Fragment).
18. Ribsiella pneumoniae.
18. Ribsiella pneumoniae.
18. Ribsiella preumoniae.
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Giffard J.M., Brandon R.B., Bell T.K.;
Giffard J.M., Brandon R.B., Bell T.K.;
"Further identification of single nucleotide polymorphisms in the equine transferrin gene.";
submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
NCBL_TaxID=9796;
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5.4e+02;
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EMBL; AE009770; AAL62822.1; -..
Hypothetical protein; Complete proteome.
SEQUENCE 35 AA; 3934 MW; A324B4F94F6A14BB CRC64;
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Q9TQR7;
01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transferrin (Fragment).
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Pred. No. 5.6e+02;
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GO; GO:0006879; F:iron ion homecetasis; IEA.
GO; GO:0006826; F:iron ion transport; IEA.
InterPro; IPR001156; Transferrin.
                                                                                                                                                       DB 95.0%; Score 19; DB Similarity 100.0%; Pred. No. 5.4 4; Conservative 0; Mismatches
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100.0%; Pre-
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EMBL; AF185722; AAF05501.1;
EMBL; AF185724; AAF05502.1;
EMBL; AF185724; AAF05503.1;
EMBL; AF185725; AAF05504.1;
EMBL; AF185725; AAF05505.1;
EMBL; AF185727; AAF05505.1;
EMBL; AF185727; AAF05505.1;
EMBL; AF185728; AAF05506.1;
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Pfam; PF00405; transferrin; 1.
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25, Created)
25, Last sequ
25, Last anno
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EMBL; AR000591; ARD07847.1; -.
PIR; E64618. E64618.
TIGR; HP0789; -.
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nes 4; Conservative
                                                    PRELIMINARY;
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01-OCT-2003 (TrEMBLre
Hypothetical protein.
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Q7UXLS;
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RESULT 9
025478
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SEQUENCE FROM N.A.
STRAIN-VS83 / ATCC 700802;
MEDLINE-2250857; PubMed-12663927;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gilli S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Kecthum K.A., Dougherty B.A., Fraser C.M.;
"Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TERMELE: 24, Last aquence update)
01-JUN-2003 (TERMELE: 24, Last annotation update)
Hypothetical protein.
BF2805.
BRITEROCOCCUS faecalis (Streptococcus faecalis).
Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
NCBI_TAXID=1351;
                      "Investigation of the Klebsiella pneumoniae 1,3-propanediol pathway: Characterization and expression of glycerol dehydratase and 1,3-propanediol oxidoreductase."; Thesis (1994), Chemical Engineering, University of Wisconsin-Madison.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 2; Length 44; 100.0%; Pred. No. 6.8e+02; ive 0; Mismatches 0; Indels
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SEQUENCE 45 AA; 5278 MW; 89CB55F5CB4C014A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000295; MIP family; 1.
Hypothetical protein; Transmembrane; Transport.
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Pfam; PF00230; MIP; 1.
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nes 4, Conserv
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Best Local Similarity
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SEQUENCE
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Q830H9

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ESULT 8

Matches

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SEQUENCE FROM N.A.
STRAIR=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
Tomb J.-F.; White O. Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F.; White D., Ketchum K.A., Klenk H.-F., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Dergo D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                             Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilomproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the gastric pathogen Helicobacter
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Planctomycetaceae, Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 19; DB 16; Length 48; 100.0%; Pred. No. 7.38+02; ive 0; Mismatches 0; Indels
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SEQUENCE 48 AA; 5492 MW; ED5911D96F57BFEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ce proteome.
60F62389C0FDA6A7 CRC64;
ol-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein HP0789.
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Last annotation update)
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EMBL; BX294135; CAD71991.1; --
Hypothetical protein; Complete proteome.
SEQUECE S1 AA, 5951 MM; 60F62389C0FDA6A7 CRC64
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Local Similarity
les 4; Conserv
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                                                                                                                                                                                                                                                              RESULT 13
QBFIF3
AC QBFIF3
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QBVSE8
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MEDLINE=210-4935; PubMed=11206551;

Perna N.T., Plunkett G. III. Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potemousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
EMEL, AE005269; AAG56425.1;
PIR; E88745; E88745.

Hypothetical protein; Complete proteome.

SEQUENCE S.4 AA; 6507 WW; BBEFACD8BE6140CE CRC64;
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"Cloning, characterization, and inactivation of the Bacillus brevis
"Cloning, characterization, and inactivation of the Bacillus brevis
J. Bacteriol. 174:2281-2287(1982).
J. Bacteriol. 174:2281-2287(1982).
PIRI, A42375; A42375.
PIRI, A42375; A42375.
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Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
NCBI_TaxID=1393;
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Escherichia coli 0157:H7.
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
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                                                                            Indels
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Last sequence update)
Last annotation update)
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Last annotation update)
                                 Pred. No. 7.8e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            52 AA
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100.08; F1
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Q44941;
01-NOV-1996 (TEMBLEEL: 01,
01-NOV-1996 (TEMBLEEL: 01,
01-JUN-2003 (TEMBLEEL: 24,
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                                 Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                     31 VAEF 34
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X3Y8
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Gaps
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STRAIN=301;
Jin O. Zhang J.Y. Liu H., Yang J., Yang F., Zhang X.B., Wang J.H.,
Jin O. Zhang J.Y. Liu H., Sun L.L., Xue Y., Zhao A.L., Gao Y.S.,
Yang G.W., Wu H.T., Dong J., Sun L.L., Xue Y., Zhao A.L., Gao Y.S.,
Yanu J.P., Kan B., Chen S.X., Yao Z.J., He B.K., Chen R.S., Ma D.L.,
Yuan Z.H., Xu J.G., Wang Y., Shen Y., Lu W.C., Qiang B.Q., Wen Y.M.,
Hou Y.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bscherichia coli O6.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Enterobacteriaceae; Shigella.
NCBI_TaxID=42897;
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SEQUENCE 54 AA; 5322 MW; 6B3C3D0F21ED4376 CRC64;
                                           01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
HJ-WAR-2003 (TrEMBLrel. 23, Last annotation update)
HJ-War-2003 (TrEMBLrel. 23, Last annotation update)
C1469.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of uropathogenic Escherichia coli.",
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
EMBL; AE016759; AAN79938.1; -.
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Pred. No. 8.2e+02;
  54 AA
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PRT;
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PRELIMINARY;
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Plasmid pCP301.
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional prediction of the coding sequences of 79 new genes deduced by analysis of cDNA clones from human fetal liver.";
Submitted (1AN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF19891; AAF69635.1. - GA33950D4657CID4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-Helicoverpa zea single nucleocapsid nucleopolyhedrovirus; Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.F., Preenail J.K., Herrmann R., Dolan M., Tingey S., Hu Z.-H., Vlak J.M.; "Genome sequence analysis of Helicoverpa zea single nucleocapsid
                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUB-Liver;
Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
He F.;
                                                                                                                                                                                                                                                                                                                                         Q9P166 PRELIMINARY, PRT; 61 AA.
09P166;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PRO2435.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4;
Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.;
"Sequence analysis of the gp37 gene of Heliothis armigera singlenucleocapsid nucleoplyhedrovirus.";
Zhongguo Bingduxue 15:35-42(2000).
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 27, Last amotation update)
01-OCT-2003 (TrEMBLrel. 25, Last amotation update)
01-OCT-2003 (TrEMBLrel. 25, Last amotation update)
0R-90 (Hypochetical protein) (Unkown).
1 Helicoverpa area single nucleocapsid nucleopolyhedrovirus, Helicoverpa armigera nucleocolyhedrovirus 64, and Helicoverpa armigera nuclear polyhedrovirus 64, and Helicoverpa armigera nuclear polyhedrosis virus.
1 Viruses; dabNA viruses, no RNA stage; Baculoviridae;
1 Nucleopolyhedrovirus.
1 Nucleopolyhedrovirus.
1 Nucleopolyhedrovirus.
                        95.0%; Score 19; DB 2; Length 61; 100.0%; Pred. No. 9.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 4; Length 61; 100.0%; Pred. No. 9.3e+02; ive 0; Mismatches 0; Indels
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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SPECIES-Heliocoverpa armigera nucleopolyhedrovirus G4;
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Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 4; Conservative
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SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4;
MEDLINE=21078302; PubMed=11210934;
Wang H., Chen X., Wang H., Arif B.M., Vlak J.M., Hu Z.;
"Nucleotide sequence and transcriptional analysis of a putative basic
DNA-binding protein of Helicoverpa armigera polyhedrovirus.";
Virus Genes 22:113-120 (2001).
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Fang M., Hu Z., Chen X., Vlak J.M.;
"Genetic organization of the HindIII-L region of Helicoverpa armigera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;
"Sequence analysis of the lap3 gene of Heliothis armigera single-
nucleocapsid nucleopolyhedrovirus.";
Zhongguo Bingduxue 15:43-49(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4; MEDLINE=21064569; PubMed=1129177; Chen X., 13Kel W.F., Tarchini R., Sandbrink H., Wang H., Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.; "The sequence of the Helicoverpa armigera single-nucleocapsid nucleopolyhedrovirus genome."; J. Gen. Virol. 82:241-257(2001).
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Sheng Wu Hua Hsueh Yu Sheng Wu Mu Li Hsueh Pao 33:179-184(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4;
Chen X., IJKel W.F., Tarchini R., Sun X., Sandbrink H., Wang
Peters S., Zuidema D., Lankhorst R. K., Vlak J. M., Hu Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h Similarity 100.0%; Score 19; DB 12; Length 68; Similarity 100.0%; Pred. No. 1e+03; 4; Conservative 0; Mismatches 0; Indels
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF334030; AALS6194.1; -.
EMBL; AF271059; AAGS3791.1; -.
EMBL; AF303045; AAK05298.1; -.
EMBL; AF303045; AAK04316.1; -.
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
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68 AA; 7962 MW; 61B7718BFBB195FF CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Helix-turn-helix protein, CopG family
NB0289.
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Gaps

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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AP005280, BAB9300.1; --
Hypothetical protein; Complete proteome.
SEQUENCE 69 AA, 7815 NW; COEZA072C2295DD2 CRC64;
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MEDLINE=22135992; PubMed=12140239;
Antunes A., Templeton A.R., Guyomard R., Alexandrino P.;
"The role of nuclear genes in intraspecific evolutionary inference: genealogy of the transferrin gene in the brown trout.";
Mol. Biol. Evol. 19:1272-1287(2002).
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01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Transferrin (Fragment).
Salmo trutta (Brown trout).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                         Corynebacterium glutamicum (Brevibacterium flavum).

Gorynebacterinae, Actinobacteridae, Actinomycetales,
Corynebacterinaee, Corynebacteriaceae; Corynebacterium.

NCBI_TaxID=1718;
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EMBL; AF4889212; AAN17073.1; JOINED.
EMBL; AF488922; AAN17073.1; JOINED.
EMBL; AF488930; AAN17078.1; JOINED.
EMBL; AF488930; AAN17078.1; JOINED.
GO; GO:0008576; C:extracellular; IEA.
GO; GO:0008199; F:ferric iron binding; IEA.
GO; GO:0006826; P:iron ion homeostasis; IEA.
InterPro; IPR001156; Transferrin.
                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
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EMBL, AF488850; AAN17027.1; JOINED.

EMBL, AF488859; AAN17027.1; JOINED.

EMBL, AF488859; AAN17037.1; JOINED.

EMBL, AF488857; AAN17037.1; JOINED.

EMBL, AF488865; AAN17037.1; JOINED.

EMBL, AF488851; AAN17037.1; JOINED.

EMBL, AF488913; AAN17042.1; JOINED.

EMBL, AF488913; AAN17042.1; JOINED.

EMBL, AF488913; AAN17068.1; JOINED.

EMBL, AF488922; AAN17073.1; JOINED.

EMBL, AF488922; AAN17073.1; JOINED.

EMBL, AF488922; AAN17073.1; JOINED.

EMBL, AF488920; AAN17073.1; JOINED.

EMBL, AF488920; AAN17073.1; JOINED.

EMBL, AF488920; AAN17073.1; JOINED.

EMBL, AF488920; AAN17078.1; JOINED.

EMBL, AF488920; AAN17078.1; JOINED.
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PRINTS; PR00422; TRANSFERIN
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SEQUENCE 71 AA; 7546 MW;
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ID Q8AUQ:
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                                                                                                          SECUENCE FROM N.A.

STRAINA-RACC 19718 / IFO 14228;

STRAINA-RACC 19718 / IFO 14228;

Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,

Hauser L., Hooper A.B., Kilotz M.G., Norton J., Sayavedra-Soto L.A.

Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;

"Complete genome sequence of the ammonia-oxidizing bacterium and

J. Bacteriol. 188:2752-2773(2003).

EMBL; BX321857; CAD84200.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
05JNBA0044M19.22 procein (OSJNBA0053B21.1 protein).
05JNBA0044M19.22 OR OSJNBA0053B21.1.
Dixaryous, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnolitophyta, Liliopsida, Poales, Poaceae;
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
NCBI_TaxID=915;
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Pred. No. 1e+03;
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1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein Cgl1907.
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100
Matches 4; Conservative
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SEQUENCE

QBNPA7; Q8NPA7 SULT 19

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Gaps

VAEF 5

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C STRAIN=Sea-1, and Sea-2;

X MEDINE=22135929; Pubmed=12140239;
Antunes A., Templeton A.R., Guyomard R., Alexandrino P.;
Antunes A., Templeton A.R., Guyomard R., Alexandrino P.;
Ty genealogy of the transferrin gene in the brown trout.";
Mol. Biol. Evol. 19:1272-1287(2002).
EMBL; AF488834; AAN17017.1; OINED.
R BMBL; AF488834; AAN17017.1; OINED.
R BMBL; AF488841; AAN17022.1; JOINED.
R BMBL; AF488841; AAN17022.1; JOINED.
R GO; GO:0005476; C:extracellular; IEA.
GO; GO:0006199; F:ferric iron binding; IEA.
GO; GO:0006199; F:ferric iron binding; IEA.
R GO; GO:000625; F:ferric iron binding; IEA.
R GO; GO:000625; F:ferric iron for transport; IEA.
R FRINTS; PR00462; TRANSFERRIN.
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STRAIN=KI2:
MEDLINE=27251358; PubMed=9097040;
MEDLINE=97251358; PubMed=9097040;
Kasai H., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
Mizobuchi K., Mori H., Mori T., Mocomura K., Nakade S., Nakamura Y.,
Mashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
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01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
101-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transferrin (Bragment).
Salmo salar (Atlantic salmon).
Salmo salar (Atlantic salmon).
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Late control gene D protein (Fragment).
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Best Local Similarity 100.
Matches 4; Conservative
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33 VAEF 36
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STRAIN=ATC 624 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Tatusto N., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL, AB007632, AAK79151.1;
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Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiam.
Clostridium.
NCBI_TaxID=1488;
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Bacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                    95.0%; Score 19; DB 2; Length 72; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0; Indels
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; D97045; D97045.
Hypothetical protein; Complete proteome.
SEQUENCE 74 AA; 8747 MW; 633633CB0A0C293A CRC64;
                                                                                                                                                                                                    SEQUENCE 72 AA; 8099 MW; 42A63B25B00EADCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CAC1179.
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01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 100.v
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Matches 4; Conservative
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097JU4;
01-OCT-2001 (
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Q82MX0
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Q97JU4
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MEDLINE=20478054; PubMed=11021991;
Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=20013326; PubMed=10544099;
Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
Lisec A.D., Nickerson K.W., Van Etten J.L.;
"Chlorella virus PBCV-1 encodes a functional homospermidine
synthase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECTEBRICE FROM N.A.
MEDLINE=96400190; PubMed=8806566;
Kutish G.F., Li Y., Lu Z., Furuta M., Rock D.L., Van Etten J.L.;
Mallysis of 76 kb of the chlorella virus PBCV-1 330-kb genome: map posttions 182 to 258.",
Virology 223:303-317(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
VCBI_TaxID=10506;
                                                                                                                                                                                                         Kleerebezem M., Boekforst J., van Kranenburg R., Molenaar D., Kleerebezem M., Boekforst J., van Kranenburg R., Molenaar D., Kleerebezem M., Boekforst J., van Kranenburg R., Mondenburg B.A., Bron P.A., Hoffer S.M., Slekem W., Klein Lankhorst R.M., Bron P.A., Hoffer S.M., Slexen R.J., Cerkhoven R., De Vries M., Chersen R.J., Complete genome sequence of Lactobacillus plantarum WGFS1."; Proc. Natl. Road. Sci. U.S.A. 100:1990-1995(2003).

BMBL; Als38257, Canb64344.1.

Hypothetical protein; Complete proteome.

SEQUENCE 77 AA, 8618 MM, CO0E2BFFID401F2F CRC64;
                                                                     Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JJM-2003 (TrEMBLrel. 24, Last annotation update)
A532L protein.
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 16; I
100.0%; Pred. No. 1.2e+03;
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STRAIN=NCIMB 8826 / WCFS1;
MEDLINE=22480296; PubMed=12566566;
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Best Local Similarity lov...
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                                                       Lactobacillus plantarum.
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Submitted (DEC-1995)
                      Hypothetical protein
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                                                                                                                   NCBI_TaxID=1590;
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Ishiwata H., Katsuma S., Kizaki K., Patel O.V., Nakano H.,
Takahashi T., Imai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y.,
Takahashi T., Imai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y.,
Taylimoto G., Izaike Y., Todoroki J., Hashizume K.;
"Characterization of gene expression profiles in early bovine
pregnancy using a custom cDNA microarray.";
Mol. Reprod. Dev. 65:9-18(2003).
EMBI. ABO89852; BACS6442.1;
Interpro; IPR003511; DNAbind_HORMA.
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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  Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitiils: deducing the ability of producing secondary metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 16; Length 74; 100.0%; Pred. No. 1.1e+03; artive 0; Mismatches 0; Indels
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                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 AA; 8832 MW; E2E1D625C848E571 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to MAD2 protein (Fragment)
Bos taurus (Bovine)
                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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SULT 25 62MB

Q88VS7 SULT 26 18VS7

79 AA.

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Gaps

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Length 77; Indels

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38 VAEF 41
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0821D2

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SEQUENCE FROM N.A.
Winans S.C., Zhu J., Oger P.M., Schrammeijer B., Hooykaas P.J.,
Farrand S.K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agrobacterium tumefaciens.
Plasmid Ti.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 12; Length 79; 100.0%; Pred. No. 1.2e+03; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Octophine-type Ti plasmid sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242881; AAF77180.1; -.
GQ; GO:0046821; C:extrachromosomal DNA; IEA.
Plasmid.
SEQUENCE 80 AA; 8723 MW; 4E8179C1100A7CA
                                                                 SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                               SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
[9]
                                                                                                                                                                           SEQUENCE FROM N.A.
Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitred (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, 142589; AAC36899.1; -.
PIR; T18034; T18034.
                             Van Etten J.L.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                           79 AA; 8698 MW; B191C627F5D5C5A7 CRC64;
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Last annotation update)
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, L)
01-JUN-2003 (TrEMBLrel. 24, L)
01-JUN-2003 (TrEMBLrel. 24, L)
BST0662 protein.
BSR0662.
Bradyrhizobium japonicum.
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
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Best Local Similarity
Matches 4; Conserv
    [6]
SEQUENCE FROM N.A.
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289WL6
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9KI36
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"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL, AP001514; BAB05901.1; -...

FIR: P3922; F83922.

Hypothetical protein; Complete protecme.

SEQUENCE 84 AA; 9669 MW; 6CDE3768ED9F5D84 CRC64;
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                                                                                                                          SEQUENCE FROM N.A.
STRAIN=USDA 110;
MEDLINE=22484999; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                     "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; ABO05937; BAC45927.1; -.
Complete proteome.
SEQUENCE 81 AA; 9235 MW; D512A9FFED0DA6C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.0%; Score 19; DB 16; Length 81; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 4; Conservative 0; Mismatches 0; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9KAV4;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein BH2182.
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Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, C.
01-JUN-2003 (TrEMBLrel. 24, L.
01-JUN-2003 (TrEMBLrel. 24, L.
Hypothetical protein.
CCA01010.
Chlamydophila caviae.
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Les 4; Conservative
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Tu G.F., Achen M.G., Aldred A.R., Southwell B.R., Schreiber G.;
"The distribution of cerebral expression of the transferrin gene is appecies specific.";
J. Biol. Chem. 266:6201-6208(1991).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ALCMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                       Stephenson S.-A., Maclean D.J., Manners J.M.;

"Disruption of a novel pathogenicity gene of Colletotrichum
"Disruption of a novel pathogenicity gene of Colletotrichum
gloeosporioides results in a hypersensitive response in the host
gloeosporioides results in a hypersensitive response in the host
submitted (MAR-1997) ro the EMBL/GenBank/DDBJ databases.

EMBL; U94183; AAB92222.1; -.

EMBL; U94183; AAB92222.1; -.

EMBL; U94183; AAB92222.1; -.

EMBL; U94183; AAB92222.1; -.

EMBL; SMOS30; HTH 3.

Fam; PF01381; HTH 3.

EMBRT; SMOS30; HTH XRZ; 1.

EYPOCHACICAL PROCECUL.
                  Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
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Similarity 100.0%; Pred. No. 1.3e+03;
4; Conservative 0; Mismatches 0; Indels
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Similarity 100.0%; Pred. No. 1.3e+03;
4; Conservative 0; Mismatches 0; Indels
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Last annotation update)
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GO; GO: 00005576; C:extracellular; IEA.
GO; GO: 0000576; C:extracellular; IEA.
GO; GO: 00006879; P:iron ion homeostasis; IEA.
GO; GO: 0006805; P:iron ion transport; IEA.
InterPro; IPR001156; Transferrin.
SMART; SM00094; IR PER; 1.
PR05IIB; PS00205; TRANSPERRIN.1; 1.
Iron transport; Metal-binding.
NON TER
NON TER
ST 97
SEQUENCE 87 AA; 9433 MW; AA464BZABDC92FAB C
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MEDLINE=91177867; PubMed=1848850;
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EMBL; M64692; AAA31586.1; -.
PIR; A38725; A38725.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
Transferrin (Fragments).
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                     NCBI_TaxID=5457;
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Q99149
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STRAIN=TW-183;
Geng M.W., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
Geng M.W., Schuhmacher A., Muehldorfer I., Melchers K.;
Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017159; AAP98704.1;
Hypothetical protein.
SRQUENCE 84 AA; 9260 MW; 7786DF8BDD7B3AB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Chlamydophila caviae (Chlamydia psitraci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae.";
Nucleic Acids Res. 31:2134-2147 (2003).
EMBL; ARO16997; AAP05749.1;
TIGR; CCA01010;
                                                                                                                                           STRAIN=GPIC;

MEDLINE-22569155; PubMed=12682364;

Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,

Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.

Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,

Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPB0775.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Racteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chiamydophila.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila
NCBI_TaxID=83557;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUT-1993 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
cingulata).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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Similarity 100.0%; Pred. No. 1.3e+03;
4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome. SEQUENCE 84 AA; 9191 MW; 7DF6009729C7093A CRC64;
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Last sequence update)
Last annotation update)
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100.0%; Pred. No. 1.3e+03;
ative 0; Mismatches 0;
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Best Local Similarity
Matches 4; Conserv
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sest Local Similarity
datches 4; Conserv
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SEQUENCE FROM N.A.
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Q7VPV6 SULT 32 VPV6

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SULT 33

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STRAIN=KIM10+;
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Q9ZGY2
RESULT 37
Q41185
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Iizumi T., Nakamura K.;

Iizumi T., Nakamura K.;

"Construction of tryptophan requiring-mutant of Nitrosomonas europaea by inactivation of tryptophan using homologous recombination.";

Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AB030031; BAA83388.1; -..

NON_TER 88 88
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                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein.
Bacteriophage PY54.
Viruses, dabba viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nitroscmonas europaea.
Bacteria; Proteobacteria; Betaproteobacteria; Nitroscmonadales;
Nitroscmonadaceae; Nitroscmonas.
NCBI_TaxID=915;
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95.0%; Score 19; DB 2; Length 88;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 4; Conservative 0; Mismatches 0; Indels
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Hertwig S.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ564013; CAD91786.1; -.
EXONUCLEASE HYPOCHELICAL protein.
SEQUENCE 87 AA; 8538 MW; D17D7A7E3075459B CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJUN-2001 (TrEMBLrel. 17, Last annotation update)
Cytochrome P460 (Fragment).
                                                                                                                                                                                                            87 AA
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Best Local Similarity 100.
Matches 4; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Shih M.C., Heinrich P., Goodman H.M.;
Cloning and chromosomal mapping of nuclear genes encoding chloroplast
and cytosolic glyceraldehyde-3-phosphate-dehydrogenase from
Arabidopsis thaliana ";
Gene 119:317-319(1993).
EMBL; 845911; ABB23533.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDLINE=99043988; PubMed=9826348;
Lindler L.E., Plano G.V., Burland V., Mayhew G.F., Blattner F.R.;
Lindler L.E., Plano G.V., Burland V., Mayhew G.F., Blattner F.R.;
Complete DNA sequence and detailed analysis of the Yersinia pestis
XIMS plasmid encoding murine toxin and capsular antigen.";
Infect. Immun. 66:5731-5742(1998).
BMBL, AROY4611; AA682761.1; -.
BMBL, AROY4611; AA682761.1; -.
BY 715018; T15018.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
InterPro; IPR003006; IG MHC.
Hypothetical protein; Plasmid.
SEQUENCE 89 AA; 10736 MW; 72B4221126023EE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                              Chloroplast.

Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                           Q41185;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Glyceraldehyde-3-phosphate-dehydrogenase subunit GapB (Fragment).
GAPB.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
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Last annotation update)
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                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress)
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PRT;
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Matches 4; Conservative
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   PRELIMINARY;
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QBIZX3;
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"The complete genome sequence of the lactic acid bacterium Lactococcus lactis spp. lactis IL1403.";

Genome Res. 11:731-753(2001).

EMBL, AE006385, AAK05648.1;

PIN, F86818; P86818.

SEQUENCE 89 AA, 10403 MW, D90DF3CF71D12D06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein ypjB.
YPDB OR L11550.
Bactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                               MEDLINE=21145866; PubMed=11248100;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AR006066; AAX02385.1; -...
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                                                                                                                                                                                  Pasteurella multocida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
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                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                             Created)
Last sequence update)
Last annotation update)
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100.0%; Pred. No. 1.3e+03;
:ive 0; Mismatches 0;
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PROSITE; PS00362; RIBOSOMAL_S15; 1.
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MEDLINE=21235186; PubMed=11337471;
                                                                                  PRT;
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ProDom; PD157043; RS15 bact; 1.
                                                                                                            01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25, 1
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                                                                                  PRELIMINARY;
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3 VAEF 6
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                                                                                                                                                                                                                            NCBI_TaxID=747;
                                                                                                                                                                                                                                                                      STRAIN=Pm70
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                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Length 89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yin F., Fan D.M.;

Yin F., Fan D.M.;

"Identifying a new variant of MAD2L1.";

Submitted (UN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF394735; AAN74648.1;

InterPro; IPR003511; DNAbind HORMA.

PÉam; PF02301; HORMA; 1.

PROSITE; FS50815; HORMA; 1.

SEQUENCE 90 AA; 10335 MW; 8209F5A7A7D8D09B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Preproinsulin (Fragment)
Ambloplites rupestris (Rock bass).
                                                                                                                                                                                                                                                                                                         01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 25, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
MAD2 mitotic arrest deficient-like 1 variant.
95.0%; Score 19; DB 16; 100.0%; Pred. No. 1.3e+03; ive 0; Mismatches 0;
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GO; GO:0005179; F:hormone activity; IEA.
GO; GO:0007582; P:physiological processes; IEA.
InterPro; IPR004825; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
PRINTS; PR00077; INSULINB.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                90 AA.
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     Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Query Match
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Q89WX7
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SCHAIN=CE3;
SCHAIN=CE3;
Forevallos M.A., Izquierdo J., Porta H., Tun C., Davila G., Brom S.,
"Rhizobium etli CE3 contains at least three plasmids of the RepABC
family: A structural and an evolutionary analysis.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF313446; AAM88940.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
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01-070-1998 (TrEMBLrel. 06, Last sequence update)
01-070-1998 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Aquaporin 1 (Fragment).
0ryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; (Dordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Plasmid p42b.
Batceria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                             Query Match

95.0%; Score 19; DB 13; Length 91;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels
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                                                            91 AA; 10100 MW; E86C8B256DC69D39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2002 (TrEMBLrel. 22, Created)
1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0TT-2003 (TrEMBLrel. 24, Last amnotation update)
Putative transcriptional regulator (Fragment).
                                                                                                                                                                                                                                                                                                                                       94 AA
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PROSITE; PS00262; INSULIN; 1.

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SEQUENCE
                                                              SEQUENCE
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Q8KY12;
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046425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The genome of the natural genetic engineer Agrobacterium tumefaciens {\sf C58."}_i,
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
VCBI_TaxID=176299;
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GO; GO:0005741; C:mitochondrial outer membrane; IEA.

GO; GO:0015288; F:porin activity; IEA.

GO; GO:0005215; F:transporter activity; IEA.

R GO; GO:0005410; P:transport; IEA.

R Ffam; PF00201; MIP; 1.

R Prodom; PD002029; MIP_family; 1.

R Prodom; PR00221; MIP; 1.

R Prodom; Transmembrane; Transport.

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NON_TER 1 4 94

SEQÜENCE 94 AA; 10057 MW; 963D552763IEBCDC CRC64;
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PIR, AB3053; AB3053.
PYP, AB3051, AB3053.
SEQUENCE 96 AA; 11193 MW, FBD635894B46ABAE CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atu4039.
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Last annotation update)
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conserv
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Hepatitis A. virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Hepatovirus.
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InterPro; IPR007138; ABM.
Pfam; PF0392; ABM; 1.
Hypothetical protein; Compl.
SEQUENCE 97 AA; 10979 MW
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Best Local Similarity ان،۰
امار 4; Conservative
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les 4; Conserv
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                                                  NCBI_TaxID=12092;
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Q8Y476;
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Matches
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                                                                                                                     MEDLINE-22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                             "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";

Bradyrhizobium japonicum USDA110.";

BMBL, AP005936; BAC4216.1;

GO, GO:0016020; C:membrane; IEA.

InterPro; IPR003425; Unk_YGGT.

Complete proteome.

SEQUENCE 96 AA; 10976 MW; A9E11F9AA4BC7734 CRC64;
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STRAIN=Vol / DSW 3638 / ATCC 43587 / JCM 8422;
STRAIN=Vol / DSW 3638 / ATCC 43587 / JCM 8422;
STRAIN=Vol / DSW 3638 / ATCC 43587 / JCM 8422;
Wheise R.B., Dunn D.M., Robb F.T., Brown J.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; ABO10262; AAL81744.1, .
Hypothetical protein; Complete proteome.
SEQUENCE 96 AA; 10804 MW; D6DAE09D096D577A CRC64;
               Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
VCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                 Query Match

95.0%; Score 19; DB 16; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein PF1620.
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Last sequence update)
Last annotation update)
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Q86535 (01-NOV-1996 (TERMELREL) 01, Cr
01-NOV-1996 (TERMELREL) 01, La
01-UUN-2001 (TERMELREL) 17, La
2C/3A (Fragment).
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Best Local Similarity 100...
4; Conservative
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SEQUENCE FROM N.A.
STRAIN=USDA 110;
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NCBI_TaxID=2261;
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UOG9
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SEQUENCE FROM N.A.
STRAIN=LGB/S;
MEDLINE=203488833, PubMed=1668326;
Fineschi N., Cavalieri F., Garelick H., Prugnola A., Pellegrini V.,
Zuckerman A.J.;
"Characterization of a hepatitis A virus strain suitable for vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      Length 97;
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1639;
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97 97
97 AA; 10614 MW; D207F7CB93110DDF CRC64;
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97 AA; 10979 MW; 9E758586E94218E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein lmo2579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 AA
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MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                              J. Hepatol. 13:S146-S151(1991).
EMBL, S44109; AAB22740.2; -.
NON TER 1 1 1 1 1 NON_TER 97 97
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Indels

Pred. No. 1.5e+03;

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4; Conservative
Best Local Similarity
Matches 4; Conserv
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Q82UR2;
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Q82UR2
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STRAIN=DC3000;
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Bodson R., Utterback T., Van Aken S., Feldilyum T., Gwinn M.,
Bodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinhac L., Fasaar C., Collmer A.,
"Complete sequence of Pseudomonas syringae.";
Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AR018862; AR05328.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATC 15692 / PA01;
STRAIN-ATC 15692 / PA01;
Strover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowallik D.J., Lagrou M.,
Bickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowallik D.J., Lagrou M.,
Brody L.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical protein.
Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonadacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
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3 AA; 10504 MW; 62836007E4849392 CRC64;
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99 AA; 10609 MW; 3AD945F44D54A85C CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PA3202.
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                                                                                                                   99 AA
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Pfam, PF03795; YCII; 1.
Hypothetical protein; Compl.
SEQUENCE 99 AA; 10609 MM
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Pfam; PF03795; YCII; 1.
Hypothetical protein; Compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       opportunistic pathogen.";
Nature 406:959-964(2000).
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                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
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Best Local Similarity
4; Conserve
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     ESULT 50
9HZ38
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Score 19; DB 16; Length 99;

95.0%;

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STRAIN=ATCC 55739;
Nam S.J., Kim J.H.;
Nam S.J., Kim J.K.;
Park J.Y., Ha Y.L., Kim J.H.;
Nam S.J., Kinad.K.;
Park J.Y., Ha Y.L., Kim J.H.;
Nam S.J., Kinad.K.;
Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
EMBL. AF401482; AAA60142.1;
EMBL. AF401482; AAA60142.1;
EMBL. AF401481;
Firtrainalation elongation factor activity; IEA.
GO; GO:0006414; Firtrainalational elongation; IEA.
InterPro; IPR01816; EF_TS.
InterPro; IPR01816; EF_TS.
InterPro; IPR01896; EF_TS; 1.
SEQUENCE 101 AA; 11650 MW; BECF30D941DB2B9B CRC64;
                                                                       Gaps
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D. Bacteriol. 185.2759-2773(2003).

EMBL, BX321861; CAD85330.1;

InterPro; IPR005545; YCII.

Hypothetical protein; Complete proteome.

EXEQUENCE 100 Aa; 10836 MW; 82DC1153BABFAE27 CRC64;
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Lactobacillus.
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OBVS54;
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 1.5e+03;
ive 0; Mismatches 0;
                                                                           Mismatches
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STRAIN=ATCC 19718 / IFO 14298;
MEDLINE=22586410; PubMed=12700255;
100.001 ° 10
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24,
25,
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Matches 4; Conservative
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                                                                                                                                                                                                                         62 VARF 65
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01-JUN-2003 (
01-OCT-2003 (
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Q9F368;
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STRAIN-ATCC 35092 / DSM 1617 / P2;
STRAIN-ATCC 35092 / DubMed=11427726;
She Q., Singh R.K., Confalonteri F., Zivanovic Y., Allard G.,
She Q., Singh R.K., Confalonteri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.",
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T., Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
                                                                                                                                                                                                                                                                                                                       Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
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            Length 101;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=198094;
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Pfam; PF02647; DUF196; 1.
TIGRPAMS; TIGR01573; cas2; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 101 Aa; 11936 MW; A7C338AD76202E17 CRC64;
                                                                                                                                                                                                                           01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SSO1404.
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
          Score 19; DB 2; L Pred. No. 1.5e+03;
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EMBL; AE006755; AAK41639.1; -.
PIR; H90297; H90297.
95.0%; Scor.
100.0%; Pred. No. 1....
'... 0; Mismatches
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MEDLINE=22608414; Pubmed=12721629;
                                              Conservative
                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                Sulfolobus solfataricus,
       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                            62 VAEF 65
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2287;
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1R27
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7YC2
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Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
Fraser C.M.,
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
BXISOC2.6 (Putative novel protein similar to APOBEC1 (Apolipoprotein BKISOC2.6.)
BXISOC2.6.
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                                                                                                                                                            "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
Nature 423:81-86(2003).
BMBL; AE017031; AAP26109.1; -.
TIGR; BA2232; -.
Hypotherical protein; Complete proteome.
SEQUENCE 102 AA; 11925 MW; 13B8E296C8A341B1 CRC64:
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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STRAIN=831(2) / M145;
MEDLINE=21994410; PubMed=12000953;
Bentley S.D., Chacer K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 13, Last annotation update)
01-MAR-1031 (TrEMBLrel. 23, Last annotation update)
SCO4420 OR SC6F11.18.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae, Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TAXID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 102;
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Pred. No. 1.5e+03;
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AL022318; CAB45276.1; -
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0;
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MEDLINE=22592660; PubMed=12705866;
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Matches 4; Conservative
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Matches 4, Conservative
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    SEQUENCE FROM N.A.
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Q8SVK0
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Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genomic sequence of nitrogen-fixing symbiotic bacterium bradythicobium japonicum USDA110.";
DNA Res. 9:189-197(2020).
EMBL; AP005950; BAC49378.1; -.
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Whoobacteriophage Barnyard.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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                                                                                                                        "Complete genome sequence of the model actinomycete Streptomyces
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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100.0%; Pred. No. 1.5e+03;
Live 0; Mismatches 0; Indels
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Nature 417:141-147(2002).
EMBL, AL939120, CACOBA29.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 103 AA; 11387 MW; 55C2B80589EB75B5 CRC64;
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100.0%; Pred. No. 1.5e+03;
ative 0; Mismatches 0;
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last anno
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conservative
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Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Frensier G. Barbe V., Peyrettaillade E., Brottier P., Wincker P.,
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weisenbach J., Vivares C.P.;
"Genome sequence and gene compaction of the eukaryote parasite
Encephalitozoon cuniculi.";
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Mycobacteriophage Corndog.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=205875;
Pedulia M.L., Ford, M.E., Houtz J.M., Karthikeyan T., Wadsworth C Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R., Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S., Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W., Hatfull G.F.; Hendrix R.W., Hatfull G.F.; Hendris of highly mosaic mycobacteriophage genomes."; Cell 113:171-182(2003) AAN02111.1; -. BRBL, AX120339; AAN02111.1; -.
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NCBL_TaxID=6035;
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100.0%; Pred. No. 1.6e+03;
iive 0; Mismatches 0; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL, ALS90445; CAD26596.1; -.
Hypothetical protein.
SEQUENCE 105 AA; 11897 MW; 08059108C05D3BB9 CRC64;
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Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ECU05_0770.
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100.0%; Pred. No. 1.6e+03;
ive 0; Mismatches 0;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CVT-2003 (TrEMBLrel. 17, Last annotation update)
Matrilyain (Fragment).
Ovis aries (Sheep).
Ovis aries (Sheep).
Mammalia: Butheria: Creation Craniata; Vertebrata; Euteleostomi;
Mammalia: Butheria: Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                            Kessler P.S., McLarnan J., Leigh J.A.;
"Nitrogenase phylogeny and the molybdenum dependence of nitrogen fixation in Methanococcus maripaludis.";
J. Bacteriol. 179:541-543 (1997).
EMBL; U75887; AAC45519.1;
PIR; T10097; T10097.
InterPro. IPR0037131. DUF153.
Fram; PF02579; Nitro FeMo-Co; 1.
SEQUENCE 106 AA; I1862 MW; 4734D89CFED33F3B CRC64;
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TISSUE=Endometrium;
A Smith G, W., Ricke W.A., Cassar C.A., Smith M.F.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF267158; AAG59846.1;
EMBL; AF267158; AAG59846.1;
EMBSP; POS237; 1MMQ.
MEROPS; MIO.0085.-
GO; GO:000422; F:metalloendopetidase activity; IEA.
GO; GO:000422; F:metalloendopetidase activity; IEA.
GO; GO:000422; F:metalloendopetidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001818; Pept MIOA MI2B.
RIMTER PR00138; MATRIXIN.
SMART; SM00235; ZnMc; 1.
NON TER
106 AA; 11578 MW, EBDE271054928018 CRC64;
SEQÜENCE 106 AA; 11578 MW, EBDE271054928018
                                                                                                                                                                     MEDLINE=96011360; PubMed=7592322;
Blank C.E., Kessler P.S., Leigh J.A.;
Genetics in methanogens: transposon insertion mutagenesis Methanococcus maripaludis niffl gene.";
J. Bacteriol. 177:5773-5777 (1995).
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        Archaea; Euryarchaeota; Methanococci; Methanococcalea;
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MEDLINE=97144542; PubMed=8990309;
MATATNAN J., Leigh
                                  Methanococcaceae, Methanococcus.
NCBI_TaxID=39152;
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                                                                                                                SEQUENCE FROM N.A. STRAIN=LL;
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STRAIN-JCM 10545 / 7;
MEDLINE-21456156; PubMed=11572479;
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MEDLINE-21456156; PubMed=11572479;
MEDLINE-21456156; PubMed=11572479;
MEDLINE-214656156; PubMed=11572479;
MEDLINE-214656156; PubMed=11572479;
Magai Y., Mishijima K., Otsuka H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka H., Makazawa H., Takamaya M., Kato Y., Yoshizawa T., Kuschi H., Yamagai M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.,
Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain?...
Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain?...
DNA Res. 8:123-146(2001).
EMBL; AP000988; BAB67095.1; -
InterPro; IPR006783; Transposase 29.
Fram; PP04693; Transposase 29.
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[1]
SEQUENCE FROM N.A. Made=12705866;
MEDLINE=22592660; PubMed=12705866;
Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C., Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pamnuzio N.R., Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S., Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W., Hatfull G.P., Carigins of highly mosaic mycobacteriophage genomes.";
Cell 113:171-182(2003).
EMBL; AX129335; AAN01935.1; -. SEQUENCE 105 AA; 11955 WW; 7D0EC09F5F2AF2DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                              Length 105;
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01-DEC-2001 (TEMBLrel. 19, Created)
01-DEC-2001 (TEMBLrel. 19, Last sequence update)
01-UJW-2003 (TEMBLrel. 24, Last annotation update)
Hypothetical protein ST2000.
ST2000
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Last sequence update)
Last annotation update)
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Methanococcus maripaludis.
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Sest Local Similarity 100.
Matches 4; Conservative
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SULT 63 1530 P71530

106 AA

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SEQUENCE FROM N.A.
STRAIN=cv. Columbia,
Federspiel N.A., Conway A.R., Davis K., Brendel V.,
Federspiel N.A., Conway A.B., Chung E., Kurtz D.B., Buehler E.,
Denwar K., Feng J., Kim C., Li Y., Shinn P., Sun H., Oji O.,
Osborne B., Shen Y.K., Toriumi M., Vyotskaia V., Yu G., Theologis A.,
                                                                                                                                                                                         01-JAN'1998 (TrEMBLrel. 05, Created)
01-JAN'1998 (TrEMBLrel. 05, Last sequence update)
01-JAN'1998 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cathepsin B-like cysteine proteinase (Fragment).
T7123.13.
T7123.13.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eucrosids II, Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
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"Genomic sequence of Arabidopsis BAC T7123.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; 199595; AAC24377.1; -
NON_TER 106 106
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                                                                                                                                         PRELIMINARY;
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Best Local Similarity
Matches 4; Conserv
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01-JUN-2001
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative thioredoxin G6G8.7. 107 AA PRELIMINARY;

2 VAEF 5

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Gaps ö 40

RESULT 68 QBNRX6

STRAIN=74-0R23-1A;

MEDINE=21135672; PubMed=11238395;

Bean L.E., Dvorachek W.H. Jr., Braun E.L., Errett A., Saenz G.S.,

Giles M.D., Werner-Washburne M., Nelson M.A., Natvig D.O.;

"Analysis of the pdx-1 (snz-1/sno-1) region of the Neurospora crassa
"Analysis of the pdx-1 (snz-1/sno-1) region of the Neurospora crassa
genome. Correlation of pyridoxine-requiring phenotypes with mutations
in two structural genes.;
Genetics 157:1067-1075(2001).

GENEL, AF319689; ARXO7845.1;
HSSP; P80028; 1TOF. Neurospora crassa. Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora. HSSP; P80028; ITOF.

OC GO:0005489; Fielectron transporter activity; IEA.

GO, GO:0006118; P:electron transport; IEA.

InterPro; IPR006662; Thiored.

InterPro; IPR006653; Thioredox.

Pfam; PF00085; thiored; IP.

PRINTS; PR00421; THIOREDOXIN. SEQUENCE FROM N.A. NCBI_TaxID=5141;

ö ö MEDINE=22255705; PubMed=1236864;
MEDINE=22255705; PubMed=1236864;
Gardner M.J. Hall N. Fung E., White O., Berriman M., Hyman R.W.,
Garlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Ghan M.-S., Mene V., Shallom S.J., Subl. B., Peterson J., Angluoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdya A.B.,
Martin D.M.A., Pairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
Werder J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Praser C.M., Barrell B.; Gaps ö ö Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium. NCBL_TaxID=36329; 95.0%; Score 19; DB 3; Length 107; 100.0%; Pred. No. 1.6e+03; ive 0; Mismatches 0; Indels 95.0%; Score 19; DB 5; Length 107; 100.0%; Pred. No. 1.6e+03; ive 0; Mismatches 0; Indels Genome sequence of the human malaria parasite Plasmodium ENEL; AEC14842; AAN36066.1; -. Hypothetical protein. SEQUENCE 107 AA; 12714 MW; CA351258FCF46EF5 CRC64; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) 107 Plasmodium falciparum (isolate 3D7) Local Similarity 100. 4; Conservative PRELIMINARY; Nature 419:498-511(2002) Hypothetical protein. Query Match Best Local Similarity Matches 4; Conserv SEQUENCE FROM N.A. 2 VAEF 5 falciparum. STRAIN=3D7 Query Match Q81HV3 RESULT 67 QBIHV3 셤

"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP062776; BAB98308.1; -.
InterPro; IPR07138; ABM. Corynebatterium glutamicum (Brevibacterium flavum). Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium. 01-0CT-2002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) SEQUENCE FROM N.A. STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025; 107 AA PRELIMINARY; Uncharacterized ACR. Nakagawa S.; QBNRX6; QBNRX6

CF4E6EAF85BE3776 CRC64;

e center. 107 AA; 11676 MW;

Redox-active SEQUENCE 10

us-09-594-978a-3.rspt

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Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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Q7TX28;
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STRAIN=H37Rv;
MEDLINE=98295937; PubMed=9634230;
Cole S.T. Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Biglmeler K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Devlin K., Peltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Retinol binding protein (Fragment).
Crocodylus niloticus (Nile crocodile) (African crocodile).
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauzia; Crocodylidae; Crocodylinae; Crocodylus.
                                                                                                                                                                                                                                                                                                                                                                                                     Hughes S., Zelus D., Mouchiroud D.;
Hughes S., Zelus D., Mouchiroud D.;
Hughes S., Zelus D., Mouchiroud D.;
Warm-blooded isochors etructure in nile crocodile and turtle.";
Wol. Biol. Evol. 16.11521-1527(1999).
BMBL; AJ011392; CABS6418.1, -
HSSP; PO2753; IRBP.
GO; GO:0005215; F:transporter activity; IEA.
InterPro; IPR002345; Lipocalin.
InterPro; IPR00266; Lipocalin.
Pfam: PF0061; lipocalin; 1.
PRINTS; PR00179; LIPOCALIN.
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Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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                             Length 107;
                                                           0; Indels
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12373 MW; B5ACF23621078018 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JOCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Rv3183.
Rv3183 OR MTV014.27 OR MT3275.
Mycobacterium tuberculosis.
                          95.0%; Score 19; DB 16; Lilarity 100.0%; Pred. No. 1.6e+03; Conservative 0; Mismatches 0;
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                          Query Match
Best Local Similarity
Matches 4; Conserv
107 AA;
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                                                                                                                       22 VAEF 25
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22709107; PubMed=12788972; Medina N., Mansoor H., Garnier T., Eldjmeler K., Camus J.-C., Medina N., Mansoor H., Garnier T., Eldjmeler K., Camus J.-C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; Pryc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; beciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021646; CA216648.1; -.
EMBL; AE0071440; AAK47615.1; -.
PIR; E70949; E70949.
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TUB-roullist; Rv3183; -.
Tubercullist; Rv3183; -.
GO; GO003677; F:DNA binding; IEA.
InterPro; IPR001387; HTH 3.
Ffam; PF01381; HTH 3; 1.
SWART; SWO0530; HTH XRE; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 109 AA; 11802 MW; A66DBE160D79613A CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible transcriptional regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 16; L
100.0%; Pred. No. 1.6e+03;
ative 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+03;
tive 0; Mismatches 0;
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Pyrococcus furiosus.
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NCBI_TaxID=2261;
                               73 VAEF 76
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2 VAEF 5
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Q8U296;
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                                                                                  RESULT 74
Q8U296
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                                                                                                                                                                                                                                            Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
Arandom DNA Sequencing, Computer-Based Approach for the Generation
of a Gene Map of Mollusum Contagiosum Virus.";
Virus Genes 0:0-0(1997).
EMBL; U86919; AABS7977.1; -.
NON_TER 110 110
NON_TER 110 110
SEQÜENCE 110 AA; 11856 MW; 6AE9GE25FC3DB780 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE=22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Chris Lee K., Kosack D., Moestl D., Wedder H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                          Oli343 PRELIMINARY; PRT; 110 AA.
Oli343,
Oli40-1997 (TrEMBLrel. 04, Created)
Ol-JUL-1997 (TrEMBLrel. 04, Last sequence update)
Ol-JUL-1997 (TrEMBLrel. 19, Last sequence update)
X1-5 protein (Fragment).
Molluscum contagiosum virus subtype 1 (MCVI).
Viruses; dSDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
NOLLUSCUM CASTONINA (MARCON).
NOLLUSCUM CASTONINA (MARCON).
NOLLUSCUM CASTONINA (MARCON).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 12; Length 110; 100.0%; Pred. No. 1.6e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                           1 1
110 110
110 AA; 11856 MW; 6AE9CE25FC3DB780 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
YCII-related domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas putida (strain KT2440).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR005545; YCII.
Pfam; PF03795; YCII; 1.
Complete proteome.
SEQUENCE 110 AA; 11775 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
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QBBEG3;
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Matches
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sluder A.; Explosive lineage-specific expansion of the orphan nuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa, Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                            P SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;

STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;

A Weiss R.B., Dunn D.M., Robb P.T., Brown J.R., I'm complete complete sequence of the Pyrococcus furiosus genome.";

I "The complete sequence of the Pyrococcus furiosus genome.";

EMBL; AE010208; AAL81087.1; -..

R InterPro; IRRO07842; HEBPN.

R PROSITE; PS50910; HEPN; 1.

R HYDOCHETICAL DIOTEIN; Complete proteome.

W HYDOCHETICAL JAA; 13379 MW; CGA005A6B2B6CA4B CRC64;
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Robinson-Rechavi M., Maina C.V., Gissendanner C.R., Laudet V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 17; Length 111; 100.0%; Pred. No. 1.7e+03; Live 0; Mismatches 0; Indels
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95.0%; Score 19; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HNP4 in nematodee.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, 7x204162; Ax039166.1;
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR008946; Str_ncl_receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Nuclear receptor NHR-1 (Fragment)
                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PF0943.
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Best Local Similarity 100.0
Matches 4; Conservative
PRELIMINARY;
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